

STIC Database Tracking Number: 228790

To: PATRICIA DUFFY
Location: REM-3B05 / Mailbox 3C18
Art Unit: 1645
Thursday, June 28, 2007

Case Serial Number: 09/955502

From: HUGH YOUNG
Location: EIC 1600
REM-1D58 / REM-1A64
Phone: (571)272-5722

hugh.young2@uspto.gov

Search Notes

Examiner Duffy,

See attached results.

If you have any questions about this search feel free to contact me at any time.

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Hugh P. Young Ph.D.
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72448

STIC-Biotech/ChemLib

6-1051

228790

From: Duffy, Patricia
Sent: Friday, June 22, 2007 6:24 PM
To: CAFE STIC-Biotech/ChemLib
Subject: sequence search

Importance: High

IN RE:09/955,502

Please search SEQ ID NO:11.

Please include a commercial and interference database search.

Please PRINT OUT top 25 hits and deliver to examiner.

11-aa 91
Patricia A. Duffy, Ph.D.

Primary Patent Examiner

571-272-0855,

Remsen 3B05,

Mailbox: 3C18

Mg

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

P

GenCore version 6.2.1

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OM protein - protein search, using sw model

Run on: June 27, 2007, 11:05:06 ; Search time 39 Seconds
(without alignments)
224.506 Million cell updates/sec

Title: US-09-955-502A-11

Perfect score: 486

Sequence: 1 MSRTFCTFLQREAGQDFQ.....NFLFEGKEVHIEGYTPEDKK 91

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

Database :

PIR 80.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	486	100.0	91	2	A85954	hypothetical prote
2	486	100.0	91	2	A85082	hypothetical prote
3	486	100.0	91	2	F91108	hypothetical prote
4	469	96.5	91	2	AH0879	conserved hypotet
5	402	82.7	90	2	C82320	conserved hypotet
6	396	81.5	90	2	AI0116	conserved hypotet
7	387	79.6	90	2	C64013	hypothetical prote
8	265	54.5	93	2	E84994	hypothetical prote
9	231	47.5	90	2	H83003	conserved hypotet
10	226	46.5	105	2	C82624	conserved hypotet
11	213	43.8	88	2	H81014	conserved hypotet
12	78	16.0	507	2	C81063	fumarate hydratase
13	78	16.0	546	2	A81807	fumarate hydratase
14	76	15.6	548	2	AS4510	63K antigen - nema
15	75.5	15.5	1638	2	D87749	protein unc-73b [l
16	75.5	15.5	2488	2	T42739	guanine nucleotide
17	74.5	15.3	683	2	AC2256	hypothetical prote
18	72	14.8	265	2	T46013	hypothetical prote
19	72	14.8	447	2	T15527	hypothetical prote
20	72	14.8	507	2	A83105	probable fumarase
21	72	14.8	511	2	A99574	ABC transporter at
22	69	14.2	258	2	A97991	hypothetical prote
23	69	14.2	258	2	E95121	phosphoesterase, p
24	69	14.2	548	2	A28209	60K filarial antig
25	69	14.2	1119	2	T15842	hypothetical prote
26	68	14.0	2672	2	A48126	translation activa
27	67.5	13.9	209	2	I64172	hypothetical prote
28	67	13.8	235	2	G65212	hypothetical 26.7K
29	67	13.8	324	2	T05429	hypothetical prote

30	67	13.8	433	2	A70465	probable GTP bindi
31	67	13.8	447	2	JC2076	alpha-1,3-mannosyl
32	66.5	13.7	544	2	T40058	probable chromatin
33	66.5	13.7	1260	2	T04440	hypothetical prote
34	66	13.6	593	2	C64097	probable soluble l
35	66	13.6	689	2	H83902	beta-galactosidase
36	65.5	13.5	173	2	H86869	hypothetical prote
37	65.5	13.5	305	2	A75211	asparaginase [EC 3
38	65.5	13.5	323	2	A90536	lipoprotein (impor
39	65.5	13.5	365	2	B54128	Fe-binding protein
40	65.5	13.5	821	2	AI2417	hypothetical prote
41	65	13.4	251	2	E90428	hypothetical prote
42	65	13.4	330	2	S74456	regulatory protein
43	65	13.4	445	1	XUHUMB	alpha-1,3-mannosyl
44	65	13.4	456	2	G71152	hypothetical prote
45	65	13.4	1008	2	H85055	probable transposo
46	65	13.4	1141	2	T29185	hypothetical prote
47	65	13.4	1230	2	S56850	SMC1 protein homol
48	64.5	13.3	245	2	AG2300	hypothetical prote
49	64.5	13.3	305	2	A71247	probable L-asparag
50	64.5	13.3	495	2	AH0985	probable zinc-prot
51	64.5	13.3	859	2	T29630	hypothetical prote
52	64	13.2	220	2	S62410	hypothetical prote
53	64	13.2	438	2	T37786	probable RNA-bindi
54	64	13.2	447	1	A38561	alpha-1,3-mannosyl
55	64	13.2	583	2	T48365	hypothetical prote
56	64	13.2	604	2	S66993	hypothetical prote
57	64	13.2	990	2	T43445	hypothetical prote
58	64	13.2	1051	2	S27002	phospholipase C (E
59	64	13.2	1234	2	S52099	phospholipase C-be
60	64	13.2	1234	2	I38994	phospholipase C-be
61	63.5	13.1	91	2	H90521	hypothetical prote
62	63.5	13.1	243	2	T29635	hypothetical prote
63	63.5	13.1	460	2	T00639	hypothetical prote
64	63.5	13.1	591	1	FOVMVM	gag polyprotein -
65	63	13.0	880	2	AE0179	probable ATPase ch
66	63	13.0	1251	2	AS6677	neuronal cell cycl
67	63	13.0	1327	2	T14594	guanidine nucleoti
68	63	13.0	1611	1	WMTMPV	183K protein - pep
69	62.5	12.9	483	1	SYBSET	glutamate-tRNA lig
70	62.5	12.9	551	2	E84106	hypothetical prote
71	62.5	12.9	555	2	C96667	unknown protein, 7
72	62.5	12.9	617	2	B71071	probable prolyl en
73	62.5	12.9	964	1	T04325	probable ATP-depen
74	62.5	12.9	1417	2	T00661	hypothetical prote
75	62	12.8	169	2	PN0560	phytochrome - long

ALIGNMENTS

RESULT 1

AB5954
Hypothetical protein yggX [imported] - Escherichia coli (strain O157:H7, substrain EDL933)
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 05-Oct-2004
C:Accession: AB5954
R:Perma, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamouisis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: AB5480, MUID:21074935; PMID:11206551
A:Accession: AB5954
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-91 <STO>
A:Cross-references: UNIPROT:P52065; UNIPARC:UPI0000163A04; GB:AB005174; NID:g12517511; P
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: yggX
C:Superfamily: fe(II) trafficking protein YggX
Query Match 100.0%; Score 486; DB 2; Length 91;

Best Local Similarity 100.0%; Pred. No. 1.6e-41;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSRTIFCTFLQREAGQDFQLYPGLGKRIYNEISKEAWAQWQHQTMLINEKKNMNA 60
DB 1 MSRTIFCTFLQREAGQDFQLYPGLGKRIYNEISKEAWAQWQHQTMLINEKKNMNA 60

QY 61 EHRKLEQEMVNFLEPGKEVHIEGYTPEDKK 91
DB 61 EHRKLEQEMVNFLEPGKEVHIEGYTPEDKK 91

RESULT 2
A65082
hypothetical protein b2962 - Escherichia coli (strain K-12)
C;Species: Escherichia coli
C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 05-Oct-2004
C;Accession: A65082
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cohen, D.; Rose, D.J.; Mau, B.; Sha, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: A65082
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-91 <BLAT>
A;Cross-references: UNIPROT:P52065; UNIPARC:UPI0000163A04; GB:AE000378; GB:U00096; NID:9
A;Experimental source: strain K-12, substrain MG1655
C;Superfamily: fe(II) trafficking protein YggX

Query Match 100.0%; Score 486; DB 2; Length 91;
Best Local Similarity 100.0%; Pred. No. 1.6e-41;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSRTIFCTFLQREAGQDFQLYPGLGKRIYNEISKEAWAQWQHQTMLINEKKNMNA 60
DB 1 MSRTIFCTFLQREAGQDFQLYPGLGKRIYNEISKEAWAQWQHQTMLINEKKNMNA 60

QY 61 EHRKLEQEMVNFLEPGKEVHIEGYTPEDKK 91
DB 61 EHRKLEQEMVNFLEPGKEVHIEGYTPEDKK 91

RESULT 3
F91108
hypothetical protein ECS3838 [imported] - Escherichia coli (strain O157:H7, substrain R)
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 05-Oct-2004
C;Accession: F91108
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.;
Gagawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gen
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: F91108
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-91 <HAY>
A;Cross-references: UNIPROT:P52065; UNIPARC:UPI0000163A04; GB:BA000007; PIDN:BA037261.1;
A;Experimental source: strain O157:H7, substrain RIMD 050952
C;Genetics:
A;Gene: ECS3838
C;Superfamily: fe(II) trafficking protein YggX

Query Match 100.0%; Score 486; DB 2; Length 91;
Best Local Similarity 100.0%; Pred. No. 1.6e-41;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSRTIFCTFLQREAGQDFQLYPGLGKRIYNEISKEAWAQWQHQTMLINEKKNMNA 60
DB 1 MSRTIFCTFLQREAGQDFQLYPGLGKRIYNEISKEAWAQWQHQTMLINEKKNMNA 60

QY 61 EHRKLEQEMVNFLEPGKEVHIEGYTPEDKK 91
DB 61 EHRKLEQEMVNFLEPGKEVHIEGYTPEDKK 91

RESULT 4
AH0879
conserved hypothetical protein STY3266 [imported] - Salmonella enterica subsp. enterica
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 05-Oct-2004
C;Accession: AH0879
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Comerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AH0879
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-91 <PAR>
A;Cross-references: UNIPARC:UPI000005A44C; GB:AL5113382; PIDN:CAD02936.1; PID:gi6504189;
C;Genetics:
A;Gene: STY3266
C;Superfamily: fe(II) trafficking protein YggX

Query Match 96.5%; Score 469; DB 2; Length 91;
Best Local Similarity 94.5%; Pred. No. 7.9e-40;
Matches 86; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSRTIFCTFLQREAGQDFQLYPGLGKRIYNEISKEAWAQWQHQTMLINEKKNMNA 60
DB 1 MSRTIFCTFLQREAGQDFQLYPGLGKRIYNEISKEAWAQWQHQTMLINEKKNMNA 60

QY 61 EHRKLEQEMVNFLEPGKEVHIEGYTPEDKK 91
DB 61 EHRKLEQEMVNFLEPGKEVHIEGYTPEDKK 91

RESULT 5
CB2320
conserved hypothetical protein VC0451 [imported] - Vibrio cholerae (strain N16961 serogr
C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 05-Oct-2004
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
chardson, D.; Ermlaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P.
1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: CB2320
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-90 <HEI>
A;Cross-references: UNIPARC:UPI00000C2CCF; GB:AE004132; GB:AE003852; NID:g9654871; PIDN:
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
C;Genetics:
A;Gene: VC0451
A;Map position: 1
C;Superfamily: fe(II) trafficking protein YggX

Query Match 82.7%; Score 402; DB 2; Length 90;
Best Local Similarity 83.3%; Pred. No. 3.6e-33;
Matches 75; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 MSRTIFCTFLQREAGQDFQLYPGLGKRIYNEISKEAWAQWQHQTMLINEKKNMNA 60
DB 1 MSRTIFCTFLQREAGQDFQLYPGLGKRIYNEISKEAWAQWQHQTMLINEKKNMNDP 60

QY 61 EHRKLEQEMVNFLEPGKEVHIEGYTPEDK 90

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Db      61 EHRKLEQEMVNFLEGGKVEHIEGYTPPAK 90
|||||
RESULT 6
A:01016
conserved hypothetical protein YPO0953 [imported] - Yersinia pestis (strain C092)
C:Species: Yersinia pestis
C>Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 05-Oct-2004
C:Accession: A10116
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, M.T.G.; Prentice, M.B.
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrall,
Nature 413, 523-527, 2001
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360
A:Accession: A10116
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-90 <KUR>
A:Cross-references: UNIPARC:UPI00000DCCC4; GB:AL590842; PIDN:CAC89796.1; PID:g15979022;
C:Genetics:
C:Superfamily: fe(II) trafficking protein YggX
Query Match      81.5%; Score 396; DB 2; Length 90;
Best Local Similarity 82.2%; Pred. No. 1.4e-32;
Matches 74; Conservative 8; Mismatches 8; Indels 0; Gaps 0;
QY 1 MSRTIFCTFLQREAGQDFQLYPGLGKRIYNEISKEAWAQHOKOTMLINEKLNMMNA 60
DB 1 MSRTIFCTFLKDAERQDFQLYPGLGKRIYNEISKEAWSQWITKOTMLINEKLSMMNI 60
QY 61 EHRKLEQEMVNFLEGGKVEHIEGYTPEDK 90
DB 61 EDRKLEQEMVNFLEGGQDVHAGITPPSK 90
RESULT 7
C64013
hypothetical protein H10760 - Haemophilus influenzae (strain Rd KW20)
C:Species: Haemophilus influenzae
C>Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 05-Oct-2004
C:Accession: C64013
R:Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.
, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.
Science 269, 496-512, 1995
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,
A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A:Reference number: A64000; MUID:95350630; PMID:7542800
A:Accession: C64013
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-90 <TIG>
A:Cross-references: UNIPROT:P40408; UNIPARC:UPI000013B0A4; GB:U32760; GB:L42023; NID:g15
C:Superfamily: fe(II) trafficking protein YggX
Query Match      79.6%; Score 387; DB 2; Length 90;
Best Local Similarity 78.2%; Pred. No. 1.1e-31;
Matches 68; Conservative 12; Mismatches 7; Indels 0; Gaps 0;
QY 1 MSRTIFCTFLQREAGQDFQLYPGLGKRIYNEISKEAWAQHOKOTMLINEKLNMMNA 60
DB 1 MARTVFCBYLKEAGLDFQLYPGLGKRIYNEISKEAWSQWITKOTMLVNEKLNMMNA 60
QY 61 EHRKLEQEMVNFLEGGKVEHIEGYTP 87
DB 61 EHRKLEQEMVNFLEGGKVDVHIEGYTP 87
RESULT 8
E84994
conserved hypothetical protein Xf1908 [imported] - Xylella fastidiosa (strain 9a5c)
C:Species: Xylella fastidiosa
C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 05-Oct-2004
C:Accession: C82624
R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
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hypothetical protein [imported] - Buchnera sp. (strain APS)
C:Species: Buchnera sp.
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 05-Oct-2004
C:Accession: E84994
R:Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
Nature 407, 81-86, 2000
A:Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. A1
A:Reference number: A84930; MUID:20445173; PMID:10993077
A:Accession: E84994
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-93 <STO>
A:Cross-references: UNIPARC:UPI000005E610; GB:AP000398; GSPDB:GN00144
A:Experimental source: strain APS
C:Genetics:
A:Gene: yggX; BU553
C:Superfamily: fe(II) trafficking protein YggX
Query Match      54.5%; Score 265; DB 2; Length 93;
Best Local Similarity 61.8%; Pred. No. 1.6e-19;
Matches 47; Conservative 16; Mismatches 13; Indels 0; Gaps 0;
QY 1 MSRTIFCTFLQREAGQDFQLYPGLGKRIYNEISKEAWAQHOKOTMLINEKLNMMNA 60
DB 17 MRRILFTFTFKKSEQDFQSYPGKLGKIKYDQISKKAWEKWIEKQITILINEENLWNL 76
QY 61 EHRKLEQEMVNFLE 76
DB 77 EHRKKIEKYMKLFLPK 92
RESULT 9
H83003
conserved hypothetical protein PA5148 [imported] - Pseudomonas aeruginosa (strain PAO1)
C:Species: Pseudomonas aeruginosa
C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 05-Oct-2004
C:Accession: H83003
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic patho
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: H83003
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-90 <STO>
A:Cross-references: UNIPARC:UPI00000C5F26; GB:AE004927; GB:AE004091; NID:g9951437; PIDN:
A:Experimental source: strain PAO1
C:Genetics:
A:Gene: PA5148
C:Superfamily: fe(II) trafficking protein YggX
Query Match      47.5%; Score 231; DB 2; Length 90;
Best Local Similarity 51.7%; Pred. No. 3.7e-16;
Matches 45; Conservative 10; Mismatches 32; Indels 0; Gaps 0;
QY 1 MSRTIFCTFLQREAGQDFQLYPGLGKRIYNEISKEAWAQHOKOTMLINEKLNMMNA 60
DB 1 MSRTVNCRKYHEELPGLDRPPYPGAKGEDIYNNVSRKAWDEWQHKOTMLINERKLNMMNA 60
QY 61 EHRKLEQEMVNFLEPGKEVHIEGYTP 87
DB 61 EDRKFLQEQMDKFLSGEDYAKADGYTP 87
RESULT 10
C82624
conserved hypothetical protein Xf1908 [imported] - Xylella fastidiosa (strain 9a5c)
C:Species: Xylella fastidiosa
C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 05-Oct-2004
C:Accession: C82624
R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
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Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen *Xylella fastidiosa*.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
A;Accession: C82624
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-105 <SIM>
A;Cross-references: UNIPARC:UPI00000C289F; GB:AE004010; GB:AE003849; NID:g9106992; PIDN:
A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
B;Ribeiro, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carreir, H
as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig
Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silv
M.; Tshuko, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A;Reference number: A59328
A;Contents: annotation
C;Genetics:
A;Gene: XF1908
C;Superfamily: fe(II) trafficking protein YggX
Query Match 46.5%; Score 226; DB 2; Length 105;
Best Local Similarity 50.6%; Pred. No. 1.4e-15;
Matches 45; Conservative 10; Mismatches 34; Indels 0; Gaps 0;
QY 1 MSRTIFCTFLQREAGQDFQLYPGELGKRIYNEISKEAWAQHOKTMLINEKLMNMA 60
Db 16 MQRIIFCEYEQRTGELDFVPYFGLGKIFACIGKVGWAALVHQTMLINENRSLPRNP 75
QY 61 EHRKLLQEMVNFLEFGKEVHIEGYTPED 89
Db 76 SHRAFLLEELNKLFLFERRVAKPEGYIEPD 104
RESULT 11
H81014
conserved hypothetical protein NMB2021 [imported] - Neisseria meningitidis (strain MC58
C;Species: Neisseria meningitidis
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 05-Oct-2004
C;Accession: H81014; F81958
R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.
ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Massignani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve
A;Title: Complete genome sequence of *Neisseria meningitidis* serogroup B strain MC58.
A;Reference number: A81000; MUID:20175755; PMID:10710307
A;Accession: H81014
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-88 <TET>
A;Cross-references: UNIPARC:UPI00000C4E7F; GB:AE002552; GB:AE002098; NID:g7227279; PIDN:
A;Experimental source: serogroup B, strain MC58
R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
Holroyd, S.; Jagsels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of *Neisseria meningitidis* Z2491.
A;Reference number: A81775; MUID:20222556; PMID:10761919
A;Accession: F81958
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-88 <PAR>
A;Cross-references: UNIPARC:UPI00000C4E7F; GB:AL162753; GB:AL157959; NID:g7379120; PIDN:
A;Experimental source: serogroup A, strain Z2491
C;Genetics:
A;Gene: NMB2021; NMA0419

C;Superfamily: fe(II) trafficking protein YggX
Query Match 43.8%; Score 213; DB 2; Length 88;
Best Local Similarity 44.3%; Pred. No. 2.2e-14;
Matches 39; Conservative 16; Mismatches 33; Indels 0; Gaps 0;
QY 1 MSRTIFCTFLQREAGQDFQLYPGELGKRIYNEISKEAWAQHOKTMLINEKLMNMA 60
Db 1 MARWVFCVCLKKAGBGMKFFPLNELGKRIYFENVSQEAWAAWTRHQTMLINENRSLADP 60
QY 61 EHRKLLQEMVNFLEFGKEVHIEGYTPED 88
Db 61 RAREYLAQQMEQYFFGADAVQGYVPQ 88
RESULT 12
C81063
fumarate hydratase, class I NMB1613 [imported] - *Neisseria meningitidis* (strain MC58 ser
C;Species: *Neisseria meningitidis*
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C;Accession: C81063
R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.
ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Massignani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve
A;Title: Complete genome sequence of *Neisseria meningitidis* serogroup B strain MC58.
A;Reference number: A81000; MUID:20175755; PMID:10710307
A;Accession: C81063
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-507 <TET>
A;Cross-references: UNIPARC:UPI00000C4759; GB:AE002511; GB:AE002098; NID:g7226857; PIDN:
A;Experimental source: serogroup B, strain MC58
C;Genetics:
A;Gene: NMB1613
C;Superfamily: iron-dependent fumarate hydratase; iron-dependent tartrate dehydratase al
Query Match 16.0%; Score 78; DB 2; Length 507;
Best Local Similarity 30.2%; Pred. No. 4.5;
Matches 19; Conservative 18; Mismatches 20; Indels 6; Gaps 2;
QY 22 YPELGKRI-YNEISKEAWAQHOKTMLINEKLMNMAEHRKLLQEMVNFLEFGKEV 80
Db 311 YSPDNGKRVDDVTKTKEEVASWKTGVDLLNGKLTGRDAHKRL-----VDMLNKGBEL 365
QY 81 HIE 83
Db 366 PVD 368
RESULT 13
A81807
fumarate hydratase (EC 4.2.1.2) NMA1812 [imported] - *Neisseria meningitidis* (strain Z2491
C;Species: *Neisseria meningitidis*
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C;Accession: A81807
R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
Holroyd, S.; Jagsels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of *Neisseria meningitidis* Z2491.
A;Reference number: A81775; MUID:20222556; PMID:10761919
A;Accession: A81807
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-546 <PAR>
A;Cross-references: UNIPARC:UPI00000C4CA5; GB:AL162757; GB:AL157959; NID:g7380371; PIDN:
A;Experimental source: serogroup A, strain Z2491
C;Genetics:
A;Gene: fuma; NMA1812
C;Superfamily: iron-dependent fumarate hydratase; iron-dependent tartrate dehydratase al
C;Keywords: carbon-oxygen lyase; hydro-lyase

Query Match 16.0%; Score 78; DB 2; Length 546;
Best Local Similarity 30.2%; Pred. No. 4.8;
Matches 19; Conservative 18; Mismatches 20; Indels 6; Gaps 2;

QY 22 YPGEIGKRT-VNEISKEAWAQOHKQTMLINEKKNMNAEHRKLLGEQEMVNFLEPGKEV 80
DB 350 YSPDNGKRVDDVKLTKEEVASWKTGVLNGKILTGDAHKKRL-----VMDLKGGEEL 404
QY 81 HIE 83
DB 405 PVD 407

RESULT 14
A54510
63K antigen - nematode (Brugia malayi)
C:Species: Brugia malayi
C:Date: 15-Oct-1994 #sequence_revision 15-Oct-1994 #text_change 09-Jul-2004
C:Accession: A54510
E:Perrine, K.G.; Denker, J.A.; Nilsen, T.W.
Mol. Biochem. Parasitol. 30, 97-104, 1988
A:Title: A multi-copy gene encodes a potentially protective antigen in Brugia malayi.
A:Reference number: A54510; MUID:88288341; PMID:2840577
A:Accession: A54510
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-548 <PER>
A:Cross-references: UNIPROT:P10723; UNIPARC:UPI00001365DE; GB:J03971; NID:GI56056; PIDN:
C:Genetics:
A:Introns: 23/2, 79/3; 140/1; 163/3; 214/1; 276/3; 321/3; 379/3; 433/3; 481/3
C:Superfamily: lysine-tRNA ligase

Query Match 15.6%; Score 76; DB 2; Length 548;
Best Local Similarity 30.7%; Pred. No. 7.7;
Matches 27; Conservative 16; Mismatches 31; Indels 14; Gaps 4;

QY 3 RTIFCTFLQREAGQDFQYPGELGKRIYNEISKEAWAQ-WQH-KQTMLINEKKNMNA 60
DB 23 RLYQAMIIITKSKGDFLIRTKDQIWEAASKTALKSKWHVEQEMLKNEKVA----- 77
QY 61 EHRKLEQEMVNF-----LPEGKEVHIE 83
DB 78 --AKMLEKDATEVGVKAALAEAKKVQIE 103

RESULT 15
D87749
protein unc-73b [imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: D87749
R:anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biology
A:Reference number: A75000; MUID:99069613; PMID:9851916
A:Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_elegans/
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A:Accession: D87749
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1638 <STO>
A:Cross-references: UNIPROT:O61528; UNIPARC:UPI000002A21C; GB:chr_I; PIDN:AAC71109.1; PI
C:Genetics:
A:Gene: unc-73b
A:Map position: 1

Query Match 15.5%; Score 75.5; DB 2; Length 1638;
Best Local Similarity 38.6%; Pred. No. 30;
Matches 17; Conservative 9; Mismatches 15; Indels 3; Gaps 1;

QY 24 GELGKRIYNEISKEAWAQOHKQTMLINEKKNMNAEHRKLL 67

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-683 <KUR>
A:Cross-references: UNIPROT:Q8YR48; UNIPARC:UPI000000CE850; GB:BA0000019; PIDN:BAB75301.1;
A:Experimental source: strain PCC 7120
C:Genetics:
C:Superfamily: Synchocystis long-chain-fatty-acid-CoA ligase; acetate-CoA ligase homolog

Query Match 15.3%; Score 74.5; DB 2; Length 683;
Best Local Similarity 28.4%; Pred. No. 14;
Matches 23; Conservative 21; Mismatches 24; Indels 13; Gaps 5;

QY 16 GDFPOLYFGLGKRIYNEISKEAWAQHQTMLI--NEKKLNMM--NAEHRKLLLEQWVNF 74
DB 568 GQDQR-----SIGALIVPNV--BALAKWAESQNLVLVSVDNDLTSSSSQINLESKMIQGL 621
QY 75 FEGKEVHIE-----GYTPEDK 90
DB 622 FR-QELNREVQNPGRVPDDR 641

RESULT 18
T46013
hypothetical protein T10K17.120 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C:Accession: T46013
R:Benes, V.; Wurmbach, E.; Drzonsek, H.; Anzorge, W.; Meves, H.W.; Lemcke, K.; Mayer, K.R.
submitted to the Protein Sequence Database, January 2000
A:Reference number: Z33019
A:Accession: T46013
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-265 <BEN>
A:Cross-references: UNIPROT:Q9M207; UNIPARC:UPI000000A3117; EMBL:AL132977
A:Experimental source: cultivar Columbia; BAC clone T10K17
C:Genetics:
A:Map position: 3
A:Introns: 42/3; 224/3; 246/3
A:Note: T10K17.120

Query Match 14.8%; Score 72; DB 2; Length 265;
Best Local Similarity 31.2%; Pred. No. 8.4;
Matches 20; Conservative 16; Mismatches 26; Indels 2; Gaps 1;

QY 8 TFLQEAEGQDFLYPGLGKRIYNEISKEAWAQHQTMLI--NEKKLNMM--NAEHRKL 65
DB 9 TGLGGAKEDEDEYMGDLISQIFPQLSQTSKRSEKTIIVPSRKKLKLNWHERR 68
QY 66 LEQE 69
DB 69 LEKE 72

RESULT 19
T16527
hypothetical protein K02F3.6 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: T16527
R:Bentley, D.
submitted to the EMBL Data Library, May 1994
A:Description: The sequence of C. elegans cosmid K02F3.
A:Reference number: Z18530
A:Accession: T16527
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-447 <BEN>
A:Cross-references: UNIPARC:UPI000017BA7D; EMBL:U000052; NID:g485125; PID:g485136; PIDN:A
A:Experimental source: strain Bristol N2
C:Genetics:
A:Gene: CESP:K02F3.6

A:Introns: 125/3; 191/3; 228/2; 322/2; 404/3

Query Match 14.8%; Score 72; DB 2; Length 447;
Best Local Similarity 32.9%; Pred. No. 15;
Matches 24; Conservative 11; Mismatches 22; Indels 16; Gaps 5;

QY 23 PGBLGKRIYNEISKEAWAQHQTMLI--NEKKLNMM--NAEHRKLLLEQWVNFLEPGEKE 79
DB 304 PGFRRKIYI-----SWSQFRKSWYFFYQNEKIPKPEMLCSADDMKMLE-----LCFRAKE 353
QY 80 VHIE---GYTPED 89
DB 354 IGIQNNKNTDED 366

RESULT 20
A83105
probable fumarate PA4333 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: A83105
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Br.
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
. J.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: A83105
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-507 <STO>
A:Cross-references: UNIPARC:UPI000000C5CC5; GB:AE004849; GB:AE004091; NID:g9950550; PIDN:
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA4333
C:Superfamily: iron-dependent fumarate hydratase; iron-dependent tartrate dehydratase al

Query Match 14.8%; Score 72; DB 2; Length 507;
Best Local Similarity 25.6%; Pred. No. 18;
Matches 20; Conservative 18; Mismatches 28; Indels 12; Gaps 3;

QY 13 EASGQDFQLYP-----GELGRI-YNEISKEAWAQHQTMLINEKKLNMM--NAEHRKL 65
DB 294 ELEAPSLDAYPEIWEAGPSARRVDLKITPEVQSWKRPGETLLNGKLTGRDAHKKR- 352
QY 66 LEQWVNFLEPGEKEVHIE 83
DB 353 ----WVDMLNKGETLPVD 366

RESULT 21
A99574
ABC transporter atp-binding protein [imported] - Mycoplasma pulmonis (strain UAB CTIP)
C:Species: Mycoplasma pulmonis
C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C:Accession: A99574
R:Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.;
Nucleic Acids Res. 29, 2145-2153, 2001
A:Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm
A:Reference number: A99512; MUID:21267165; PMID:11353084
A:Accession: A99574
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-511 <KUR>
A:Cross-references: UNIPROT:Q98Q71; UNIPARC:UPI000000D45F4; GB:AL445566; PID:g14089911; P
A:Experimental source: strain UAB CTIP
C:Genetics:
A:Gene: MYPU 4970
A:Genetic code: SGC3

Query Match 14.8%; Score 72; DB 2; Length 511;
Best Local Similarity 28.9%; Pred. No. 18;
Matches 22; Conservative 20; Mismatches 28; Indels 6; Gaps 5;

RESULT 24
A28209

Query Match 14.2%; Score 69; DB 2; Length 548;
Best Local Similarity 28.4%; Pred. No. 38;
Matches 25; Conservative 18; Mismatches 31; Indels

RESULT 25
T15842

Query M
Best Lo
Matches

Search completed: June 27, 2007, 11:11:27
Job time : 43 secs

Search completed: June 27, 2007, 11:11:27
Job time : 43 secs

GenCore version 6.2.1
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OM protein - protein search, using sw model

Run on: June 27, 2007, 10:57:23 ; Search time 215 Seconds
(without alignments)
207.113 Million cell updates/sec

Title: US-09-955-502A-11

Perfect score: 486

Sequence: 1 MSRTIFCTFLQREAGQDFQ.....NFLFEKGVHIEGYTPEDKK 91

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2782304 seqs, 489333398 residues

Total number of hits satisfying chosen parameters: 2782304

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

Database :

- A_Geneseq_200701.*
- 1: geneseqp1980s.*
- 2: geneseqp1990s.*
- 3: geneseqp2000s.*
- 4: geneseqp2001s.*
- 5: geneseqp2002s.*
- 6: geneseqp2003as.*
- 7: geneseqp2003bs.*
- 8: geneseqp2004s.*
- 9: geneseqp2005s.*
- 10: geneseqp2006s.*
- 11: geneseqp2007s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	486	100.0	91	5	Abb78158 Amino aci
2	486	100.0	91	5	Abb78157 Amino aci
3	486	100.0	91	5	Abb78156 Amino aci
4	469	96.5	91	5	Abb78161 Amino aci
5	469	96.5	91	5	Abb78159 Amino aci
6	469	96.5	91	5	Abb78162 Amino aci
7	455	93.6	91	5	Abb78163 Amino aci
8	453	93.2	88	5	Abb78160 Amino aci
9	450	92.6	107	7	Abb78160 Amino aci
10	436	89.7	126	10	Abb78160 Amino aci
11	402	82.7	90	5	Abb78155 Amino aci
12	396	81.5	90	5	Abb78165 Amino aci
13	395	81.3	78	5	Abb78164 Amino aci
14	389	80.0	93	7	Abb78158 Bacterial
15	388	79.8	91	5	Abb78150 Amino aci
16	387	79.6	87	5	Abb78152 Amino aci
17	379	78.0	87	5	Abb78151 Amino aci
18	373	76.7	87	5	Abb78153 Amino aci
19	332	68.3	80	5	Abb78154 Amino aci
20	265	54.5	76	5	Abb78166 Amino aci
21	255	52.5	87	5	Abb78148 Amino aci
22	255	52.5	87	5	Abb78147 Amino aci

23	241	49.6	86	5	ABB78149	Amino aci
24	231.5	47.6	89	9	AE941576	L. pneumo
25	231.5	47.6	95	9	AE938294	L. pneumo
26	231	47.5	87	5	ABB78170	Amino aci
27	231	47.5	122	7	ABO74609	Pseudomon
28	227	46.7	88	5	ABB78178	Amino aci
29	227	46.7	90	5	ABB78168	Amino aci
30	225	46.3	87	5	ABB78169	Amino aci
31	216.5	44.5	90	5	ABB78167	Amino aci
32	213	43.8	88	5	ABB78171	Amino aci
33	213	43.8	88	5	ABB78172	Amino aci
34	213	43.8	88	5	ABB78173	Amino aci
35	213	43.8	88	6	ABP77219	N. gonorr
36	206	42.4	87	5	ABB78175	Amino aci
37	200	41.2	87	5	ABB78177	Amino aci
38	200	41.2	87	5	ABB78174	Amino aci
39	200	41.2	87	5	ABB78176	Amino aci
40	199.5	41.0	92	6	ADA34169	Acinetoba
41	131	27.0	110	8	ADL05173	M. catar
42	83	17.1	506	3	AA747371	Neisseria
43	83	17.1	1647	4	ABG10750	Novel hum
44	81	16.7	507	6	ABU40210	Protein e
45	78	16.0	507	3	AA74372	Neisseria
46	78	16.0	507	3	AA74373	Neisseria
47	78	16.0	546	6	ABU38097	Protein e
48	76	15.6	548	4	AAE04737	Brugia ma
49	75	15.4	309	8	ADN46828	Thermococ
50	74.5	15.3	632	8	ADS29711	Bacterial
51	72	14.8	474	7	ABO75727	Pseudomon
52	71.5	14.7	102	9	AE666451	Partial r
53	71.5	14.7	222	9	AE666453	Partial r
54	71.5	14.7	679	9	ADZ85056	Partial F
55	71.5	14.7	1208	9	AE666445	Full-leng
56	71	14.6	311	7	ADM26256	Hyperther
57	70.5	14.5	285	4	AA926683	Human pro
58	70.5	14.5	414	6	ABU11747	Human MDD
59	70.5	14.5	614	9	ADX06837	Cyclin-de
60	70.5	14.5	614	9	ADY16108	PRO poly
61	70.5	14.5	764	5	ABB77432	Human tum
62	70.5	14.5	764	7	ADC99062	Human KPP
63	70.5	14.5	863	4	AA38657	Human pol
64	70.5	14.5	863	4	AA38656	Human pol
65	70.5	14.5	1135	8	ADS10706	Human the
66	70.5	14.5	1181	8	ADS10708	Human the
67	70.5	14.5	1186	8	ADS10709	Human the
68	70.5	14.5	1188	8	ADH45460	Human mol
69	70.5	14.5	1206	5	ADH48860	NOV61 pro
70	70.5	14.5	1206	5	AEJ61819	Human NOV
71	70.5	14.5	1214	7	ADK65785	Angiogene
72	69.5	14.3	374	4	AA39682	Human pol
73	69.5	14.3	389	4	AA441468	Human pol
74	69.5	14.3	481	5	AAU93169	Arabidops
75	69.5	14.3	481	7	ADD30148	Plant yie

ALIGNMENTS

RESULT 1

ABB78158

ID ABB78158 standard; protein; 91 AA.

XX ABB78158;

AC ABB78158;

XX 05-NOV-2002 (first entry)

XX Amino acid sequence of a YggX homologue.

XX Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;

XX hydroxyl radical; DNA damage; YggX homologue.

XX Unidentified.

PN US2002072118-A1.
 XX 13-JUN-2002.
 XX
 XX 18-SEP-2001; 2001US-00955502.
 XX
 XX 22-SEP-2000; 2000US-0234588P.
 XX
 XX (DOWN/) DOWNS D.
 PA (GRAL/) GRALNICK J A.
 XX
 XX Downs D, Gralnick JA;
 XX WPI; 2002-589476/63.
 XX
 XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
 PT cell, comprises engineering the cell to produce more YggX protein, a
 PT protein identified from Salmonella enterica Serovar Typhimurium.
 XX
 XX Example; Fig 1A; 16pp; English.
 XX
 XX The specification describes a method for reducing superoxide damage to a
 CC cell. The method comprises engineering the cell to produce more than the
 CC native amount of YggX protein (a protein identified from Salmonella
 CC enterica serovar typhimurium) or its homolog, where the cells are
 CC rendered more resistant to superoxide damage. YggX reduces the oxidation
 CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
 CC clusters. The resulting decrease in free-iron levels generates fewer
 CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
 CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
 CC cell. ABB78147-78 represent YggX homologues
 XX
 XX Sequence 91 AA;
 SQ
 Query Match 100.0%; Score 486; DB 5; Length 91;
 Best Local Similarity 100.0%; Pred. NO. 3.5e-48;
 Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSRTIFCTFLQREAGQDFQLYPGELGKRIYNEISKEAWAQWQHKTMLINEKLLNMNNA 60
 DB 1 MSRTIFCTFLQREAGQDFQLYPGELGKRIYNEISKEAWAQWQHKTMLINEKLLNMNNA 60
 QY 61 EHRKLEQEMVNFLEGGKEVHIEGYTPEDKK 91
 DB 61 EHRKLEQEMVNFLEGGKEVHIEGYTPEDKK 91
 RESULT 2
 ABB78157
 ID ABB78157 standard; protein; 91 AA.
 XX
 XX ABB78157;
 XX
 XX 05-NOV-2002 (first entry)
 DT
 DE Amino acid sequence of a YggX homologue.
 XX
 XX Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
 KW hydroxyl radical; DNA damage; YggX homologue.
 XX
 XX Unidentified.
 OS
 XX US2002072118-A1.
 PN
 XX 13-JUN-2002.
 PD
 XX 18-SEP-2001; 2001US-00955502.
 XX
 XX 22-SEP-2000; 2000US-0234588P.
 XX
 XX (DOWN/) DOWNS D.
 PA (GRAL/) GRALNICK J A.
 XX
 XX The specification describes a method for reducing superoxide damage to a

PI Downs D, Gralnick JA;
 XX WPI; 2002-589476/63.
 XX
 XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
 PT cell, comprises engineering the cell to produce more YggX protein, a
 PT protein identified from Salmonella enterica Serovar Typhimurium.
 XX
 XX Example; Fig 1A; 16pp; English.
 XX
 XX The specification describes a method for reducing superoxide damage to a
 CC cell. The method comprises engineering the cell to produce more than the
 CC native amount of YggX protein (a protein identified from Salmonella
 CC enterica serovar typhimurium) or its homolog, where the cells are
 CC rendered more resistant to superoxide damage. YggX reduces the oxidation
 CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
 CC clusters. The resulting decrease in free-iron levels generates fewer
 CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
 CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
 CC cell. ABB78147-78 represent YggX homologues
 XX
 XX Sequence 91 AA;
 SQ
 Query Match 100.0%; Score 486; DB 5; Length 91;
 Best Local Similarity 100.0%; Pred. NO. 3.5e-48;
 Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSRTIFCTFLQREAGQDFQLYPGELGKRIYNEISKEAWAQWQHKTMLINEKLLNMNNA 60
 DB 1 MSRTIFCTFLQREAGQDFQLYPGELGKRIYNEISKEAWAQWQHKTMLINEKLLNMNNA 60
 QY 61 EHRKLEQEMVNFLEGGKEVHIEGYTPEDKK 91
 DB 61 EHRKLEQEMVNFLEGGKEVHIEGYTPEDKK 91
 RESULT 3
 ABB78156
 ID ABB78156 standard; protein; 91 AA.
 XX
 XX ABB78156;
 XX
 XX 05-NOV-2002 (first entry)
 DT
 DE Amino acid sequence of a YggX homologue.
 XX
 XX Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
 KW hydroxyl radical; DNA damage; YggX homologue.
 XX
 XX Escherichia coli.
 OS
 XX US2002072118-A1.
 PN
 XX 13-JUN-2002.
 PD
 XX 18-SEP-2001; 2001US-00955502.
 XX
 XX 22-SEP-2000; 2000US-0234588P.
 XX
 XX (DOWN/) DOWNS D.
 PA (GRAL/) GRALNICK J A.
 XX
 XX Downs D, Gralnick JA;
 XX WPI; 2002-589476/63.
 XX
 XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
 PT cell, comprises engineering the cell to produce more YggX protein, a
 PT protein identified from Salmonella enterica Serovar Typhimurium.
 XX
 XX Example; Fig 1A; 16pp; English.
 XX
 XX The specification describes a method for reducing superoxide damage to a

CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YggX protein (a protein identified from Salmonella
CC enterica serovar typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. YggX reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
CC cell. ABB78147-78 represent YggX homologues
XX
SQ Sequence 91 AA;

Query Match 100.0%; Score 486; DB 5; Length 91;
Best Local Similarity 100.0%; Pred. No. 3.5e-48;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSRTICTFLQREAGQDFQLYPGLGKRIYNEISKEAWAQWQHKTMLINEKKLNMMNA 60
DB 1 MSRTICTFLQREAGQDFQLYPGLGKRIYNEISKEAWAQWQHKTMLINEKKLNMMNA 60

QY 61 EHRKLEQEMVNFPEGKEVHIEGYTPEDKK 91
DB 61 EHRKLEQEMVNFPEGKEVHIEGYTPEDKK 91

RESULT 4
ABB78161
ID ABB78161 standard; protein; 91 AA.
AC ABB78161;
XX
XX
DT 05-NOV-2002 (first entry)
DE Amino acid sequence of a YggX homologue.
XX
XX Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
KW hydroxyl radical; DNA damage; YggX homologue.
OS Unidentified.
XX
XX US2002072118-A1.
PN
XX
PD 13-JUN-2002.
XX
XX 18-SEP-2001; 2001US-00955502.
PF
XX 22-SEP-2000; 2000US-0234588P.
PR
XX (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
XX
XX Downs D, Gralnick JA;
PI WPI; 2002-589476/63.
DR
XX
XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from Salmonella enterica Serovar Typhimurium.
XX
XX Example; Fig 1A; 16pp; English.

The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YggX protein (a protein identified from Salmonella
CC enterica serovar typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. YggX reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
CC cell. ABB78147-78 represent YggX homologues
XX
SQ Sequence 91 AA;

Query Match 96.5%; Score 469; DB 5; Length 91;
Best Local Similarity 94.5%; Pred. No. 3.2e-46;
Matches 86; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSRTICTFLQREAGQDFQLYPGLGKRIYNEISKEAWAQWQHKTMLINEKKLNMMNA 60
DB 1 MSRTICTFLQREAGQDFQLYPGLGKRIYNEISKEAWAQWQHKTMLINEKKLNMMNA 60

QY 61 EHRKLEQEMVNFPEGKEVHIEGYTPEDKK 91
DB 61 EHRKLEQEMVNFPEGKEVHIEGYTPEDKK 91

RESULT 5
ABB78159
ID ABB78159 standard; protein; 91 AA.
XX
XX
AC ABB78159;
XX
XX 05-NOV-2002 (first entry)
DT Amino acid sequence of a YggX homologue.
XX
XX Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
KW hydroxyl radical; DNA damage; YggX homologue.
OS Unidentified.
XX
XX US2002072118-A1.
PN
XX
PD 13-JUN-2002.
XX
XX 18-SEP-2001; 2001US-00955502.
PF
XX 22-SEP-2000; 2000US-0234588P.
PR
XX (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
XX
XX Downs D, Gralnick JA;
PI WPI; 2002-589476/63.
DR
XX
XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from Salmonella enterica Serovar Typhimurium.
XX
XX Example; Fig 1A; 16pp; English.

The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YggX protein (a protein identified from Salmonella
CC enterica serovar typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. YggX reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
CC cell. ABB78147-78 represent YggX homologues
XX
SQ Sequence 91 AA;

Query Match 96.5%; Score 469; DB 5; Length 91;
Best Local Similarity 94.5%; Pred. No. 3.2e-46;
Matches 86; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSRTICTFLQREAGQDFQLYPGLGKRIYNEISKEAWAQWQHKTMLINEKKLNMMNA 60
DB 1 MSRTICTFLQREAGQDFQLYPGLGKRIYNEISKEAWAQWQHKTMLINEKKLNMMNA 60

QY 61 EHRKLEQEMVNFPEGKEVHIEGYTPEDKK 91
DB 61 EHRKLEQEMVNFPEGKEVHIEGYTPEDKK 91

```
Db      61 EHRKLEQEMVSLFEGKDVHIEGYTPEDKK 91
RESULT 6
ABB78162
ID ABB78162 standard; protein; 91 AA.
XX
AC ABB78162;
XX
DT 05-NOV-2002 (first entry)
XX
DE Amino acid sequence of a YggX homologue.
XX
DE Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
KW hydroxyl radical; DNA damage; YggX homologue.
XX
OS Salmonella typhi.
XX
PN US2002072118-A1.
XX
PD 13-JUN-2002.
XX
PF 18-SEP-2001; 2001US-00955502.
XX
PR 22-SEP-2000; 2000US-0234588P.
XX
PA (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
XX
PI Downs D, Gralnack JA;
XX
DR WPI; 2002-589476/63.
XX
PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from Salmonella enterica Serovar Typhimurium.
XX
PS Example; Fig 1A; 16pp; English.
XX
CC The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YggX protein (a protein identified from Salmonella
CC enterica serovar typhimurium) or its homologue, where the cells are
CC rendered more resistant to superoxide damage. YggX reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
CC cell. ABB78147-78 represent YggX homologues
XX
SQ Sequence 91 AA;
Query Match 96.5%; Score 469; DB 5; Length 91;
Best Local Similarity 94.5%; Pred. No. 3.2e-46;
Matches 86; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSRTIFCTFLQREAGQDFOLYPGELGKRIYNEISKAWAQWQHKTMLINEKLLNMNA 60
DB 1 MSRTIFCTYLQREAGQDFOLYPGELGKRIYNEISKAWAQWQHKTMLINEKLLNMNA 60
QY 61 EHRKLEQEMVSLFEGKDVHIEGYTPEDKK 91
DB 61 EHRKLEQEMVSLFEGKDVHIEGYTPEDKK 91
RESULT 7
ABB78163
ID ABB78163 standard; protein; 91 AA.
XX
AC ABB78163;
XX
DT 05-NOV-2002 (first entry)
XX
```

```
DE Amino acid sequence of a YggX homologue.
XX
KW Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
KW hydroxyl radical; DNA damage; YggX homologue.
XX
OS Salmonella typhimurium.
XX
PN US2002072118-A1.
XX
PD 13-JUN-2002.
XX
PF 18-SEP-2001; 2001US-00955502.
XX
PR 22-SEP-2000; 2000US-0234588P.
XX
PA (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
XX
PI Downs D, Gralnack JA;
XX
DR WPI; 2002-589476/63.
XX
PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from Salmonella enterica Serovar Typhimurium.
XX
PS Example; Fig 1A; 16pp; English.
XX
CC The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YggX protein (a protein identified from Salmonella
CC enterica serovar typhimurium) or its homologue, where the cells are
CC rendered more resistant to superoxide damage. YggX reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
CC cell. ABB78147-78 represent YggX homologues
XX
SQ Sequence 91 AA;
Query Match 93.6%; Score 455; DB 5; Length 91;
Best Local Similarity 92.3%; Pred. No. 1.4e-44;
Matches 84; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
QY 1 MSRTIFCTFLQREAGQDFOLYPGELGKRIYNEISKAWAQWQHKTMLINEKLLNMNA 60
DB 1 MSRTIFCTYLQREAGQDFOLYPGELGKRIYNEISKAWAQWQHKTMLINEKLLNMNA 60
QY 61 EHRKLEQEMVSLFEGKDVHIEGYTPEDKK 91
DB 61 EHRKLEQEMVSLFEGKDVHIEGYTPEDKK 91
RESULT 8
ABB78160
ID ABB78160 standard; protein; 88 AA.
XX
AC ABB78160;
XX
DT 05-NOV-2002 (first entry)
XX
DE Amino acid sequence of a YggX homologue.
XX
KW Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
KW hydroxyl radical; DNA damage; YggX homologue.
XX
OS Unidentified.
XX
PN US2002072118-A1.
XX
PD 13-JUN-2002.
XX
```

```
PF 18-SEP-2001; 2001US-00955502.
XX
PR 22-SEP-2000; 2000US-0234588P.
XX
PA (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
XX
PI Downs D, Gralnick JA;
XX
DR WPI; 2002-589476/63.
XX
PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from Salmonella enterica Serovar Typhimurium.
XX
PS Example; Fig 1A; 16pp; English.
XX
CC The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YggX protein (a protein identified from Salmonella
CC enterica serovar typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. YggX reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
CC cell. ABB78147-78 represent YggX homologues
XX
XX Sequence 88 AA;
XX
Query Match 93.2%; Score 453; DB 5; Length 88;
Best Local Similarity 94.3%; Pred. No. 2.2e-44;
Matches 83; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 MSRTTCTFLQREAGQDPQLYPGELGKRIYNEISKEAWAQWQHKTMLINEKLLNMNA 60
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 EHRKLLQEMWVFLPEGKEVHIEGYTPE 88
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
61 EHRKLLQEMWVFLPEGKDVIHIEGYTPE 88
XX
RESULT 9
ABO65445
ID ABO65445 standard; protein; 107 AA.
XX
AC ABO65445;
XX
XX 29-JUL-2004 (first entry)
XX
DE Klebsiella pneumoniae polypeptide seqid 11962.
XX
KW Recombinant expression vector; transcription regulatory element;
KW Klebsiella pneumoniae protein; antibacterial; Vaccine.
XX
OS Klebsiella pneumoniae.
XX
PN US6610836-B1.
XX
XX 26-AUG-2003.
XX
XX 27-JAN-2000; 2000US-00489039.
XX
XX 29-JAN-1999; 99US-0117747P.
XX
PA (GENO-) GENOME THERAPEUTICS CORP.
XX
PI Breton GL, Osborne M;
XX
DR WPI; 2003-895346/82.
DR N-PSDB; ACH98996.
XX
XX
PT New nucleic acid encoding a Klebsiella pneumoniae polypeptide, useful for
PT preparing a vaccine composition against Klebsiella pneumoniae.
XX
PS Disclosure; SEQ ID NO 11962; 932pp; English.
XX
XX The invention describes a new isolated nucleic acid encoding a Klebsiella
XX pneumoniae polypeptide. Also described are: a recombinant expression
XX vector comprising the nucleic acid, operably linked to a transcription
XX regulatory element; and a cell comprising the recombinant expression
XX vector. The nucleic acid is useful for preparing a vaccine composition
XX against Klebsiella pneumoniae. This is the amino acid sequence of a
XX Klebsiella pneumoniae polypeptide of the invention
XX
XX Sequence 107 AA;
XX
Query Match 92.6%; Score 450; DB 7; Length 107;
Best Local Similarity 91.2%; Pred. No. 6.3e-44;
Matches 83; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
XX
QY 1 MSRTTCTFLQREAGQDPQLYPGELGKRIYNEISKEAWAQWQHKTMLINEKLLNMNA 60
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 EHRKLLQEMWVFLPEGKEVHIEGYTPE 91
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
77 EHRKLLQEMWVFLPEGKDVIHIEGYTPE 107
XX
RESULT 10
AEH63450
ID AEH63450 standard; protein; 126 AA.
XX
AC AEH63450;
XX
XX 13-JUL-2006 (first entry)
XX
DE Enterobacter cloacae protein amino acid sequence - SEQ ID 9887.
XX
KW diagnosis; vaccine; bacterial infection; enterobacter infection;
KW antibacterial; screening.
XX
OS Enterobacter cloacae.
XX
XX US7041814-B1.
XX
XX 09-MAY-2006.
XX
XX 18-FEB-1999; 99US-00252691.
XX
XX 18-FEB-1998; 98US-0074787P.
XX
XX 24-JUL-1998; 98US-0094145P.
XX
XX (GENO-) GENOME THERAPEUTICS CORP.
XX
PI Weinstock KG, Deloughery C, Bush D;
XX
DR WPI; 2006-349670/36.
DR N-PSDB; AEH56055.
XX
XX New nucleic acid encoding an Enterobacter cloacae polypeptide, useful for
XX detecting, preventing, and treating pathological conditions resulting
XX from bacterial infections.
XX
PS Disclosure; SEQ ID NO 9887; 165pp; English.
XX
XX The invention comprises the amino acid and coding sequences of
XX Enterobacter cloacae proteins. The DNA and protein sequences of the
XX invention are useful for detecting, preventing, and treating pathological
XX conditions resulting from bacterial infections, and as components of
XX antibacterial vaccines. The DNA and protein sequences of the invention
XX are also useful in screening for compounds which interfere with the
XX Enterobacter cloacae life cycle or inhibit infection. The present amino
XX acid sequence represents an Enterobacter cloacae protein of the
```

```
CC invention.
XX Sequence 126 AA;
SQ

Query Match      89.7%; Score 436; DB 10; Length 126;
Best Local Similarity 88.9%; Pred. No. 3.2e-42;
Matches 80; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 MSTRTFCTFLQREAGQDFQLYPGELGKRIYNEISKEAWAQHQTMLINEKKLMMNNA 60
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
37 MARTTCTFLQREAGQDFQLYPGELGKRIYNEISKEAWAQHQTMLINEKKLMMNP 96
QY 61 EHRKLEQEMVNFLEPGKEVHIEGYTPEDK 90
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
97 EHRKLEQEMVNFLEPGKDVHIEGYTPPEK 126

RESULT 11
ABB78155
ID ABB78155 standard; protein; 90 AA.
XX AC ABB78155;
XX DT 05-NOV-2002 (first entry)
XX DE Amino acid sequence of a YggX homologue.
XX KW Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
XX KW hydroxyl radical; DNA damage; YggX homologue.
XX OS Vibrio cholerae.
XX PN US2002072118-A1.
XX PD 13-JUN-2002.
XX PF 18-SEP-2001; 2001US-00955502.
XX PR 22-SEP-2000; 2000US-0234588P.
XX PA (DOWN/) DOWNS D.
XX PA (GRAL/) GRALNICK J A.
XX PI Downs D, Gralnick JA;
XX WPI; 2002-589476/63.
XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
cell, comprises engineering the cell to produce more YggX protein, a
protein identified from Salmonella enterica Serovar Typhimurium.
XX Example; Fig 1A; 16pp; English.
XX The specification describes a method for reducing superoxide damage to a
cell. The method comprises engineering the cell to produce more than the
native amount of YggX protein (a protein identified from Salmonella
enterica serovar typhimurium) or its homolog, where the cells are
rendered more resistant to superoxide damage. YggX reduces the oxidation
of (Fe-S) clusters; and thus reduces the loss of Fe(II) ions from
clusters. The resulting decrease in free-iron levels generates fewer
hydroxyl radicals and thus reduced DNA damage. The method is useful for
reducing superoxide damage in a bacterial, yeast, mammalian or plant
cell. ABB78147-78 represent YggX homologues
XX Sequence 90 AA;
SQ

Query Match      82.7%; Score 402; DB 5; Length 90;
Best Local Similarity 83.3%; Pred. No. 1.8e-38;
Matches 75; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 MSTRTFCTFLQREAGQDFQLYPGELGKRIYNEISKEAWAQHQTMLINEKKLMMNNA 60
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 MARTVCTRLQREAGDGLDFQLYPGELGKRIYNEISKEAWAQHQTMLINEKKLMMNDP 60

CC invention.
XX Sequence 126 AA;
SQ

Query Match      89.7%; Score 436; DB 10; Length 126;
Best Local Similarity 88.9%; Pred. No. 3.2e-42;
Matches 80; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 MSTRTFCTFLQREAGQDFQLYPGELGKRIYNEISKEAWAQHQTMLINEKKLMMNNA 60
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
37 MARTTCTFLQREAGQDFQLYPGELGKRIYNEISKEAWAQHQTMLINEKKLMMNP 96
QY 61 EHRKLEQEMVNFLEPGKEVHIEGYTPEDK 90
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
97 EHRKLEQEMVNFLEPGKDVHIEGYTPPEK 126

RESULT 11
ABB78155
ID ABB78155 standard; protein; 90 AA.
XX AC ABB78155;
XX DT 05-NOV-2002 (first entry)
XX DE Amino acid sequence of a YggX homologue.
XX KW Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
XX KW hydroxyl radical; DNA damage; YggX homologue.
XX OS Vibrio cholerae.
XX PN US2002072118-A1.
XX PD 13-JUN-2002.
XX PF 18-SEP-2001; 2001US-00955502.
XX PR 22-SEP-2000; 2000US-0234588P.
XX PA (DOWN/) DOWNS D.
XX PA (GRAL/) GRALNICK J A.
XX PI Downs D, Gralnick JA;
XX WPI; 2002-589476/63.
XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
cell, comprises engineering the cell to produce more YggX protein, a
protein identified from Salmonella enterica Serovar Typhimurium.
XX Example; Fig 1A; 16pp; English.
XX The specification describes a method for reducing superoxide damage to a
cell. The method comprises engineering the cell to produce more than the
native amount of YggX protein (a protein identified from Salmonella
enterica serovar typhimurium) or its homolog, where the cells are
rendered more resistant to superoxide damage. YggX reduces the oxidation
of (Fe-S) clusters; and thus reduces the loss of Fe(II) ions from
clusters. The resulting decrease in free-iron levels generates fewer
hydroxyl radicals and thus reduced DNA damage. The method is useful for
reducing superoxide damage in a bacterial, yeast, mammalian or plant
cell. ABB78147-78 represent YggX homologues
XX Sequence 90 AA;
SQ

Query Match      81.5%; Score 396; DB 5; Length 90;
Best Local Similarity 82.2%; Pred. No. 9.1e-38;
Matches 74; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

QY 1 MSTRTFCTFLQREAGQDFQLYPGELGKRIYNEISKEAWAQHQTMLINEKKLMMNNA 60
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 MSTRTFCTFLQREAGQDFQLYPGELGKRIYNEISKEAWAQHQTMLINEKKLMMNI 60
QY 61 EHRKLEQEMVNFLEPGKEVHIEGYTPEDK 90
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
61 EDRKLEQEMVNFLEPGQDVHIEGYTPPSK 90

RESULT 13
ABB78164
ID ABB78164 standard; protein; 78 AA.
XX AC ABB78164;
```

```

XX DT 05-NOV-2002 (first entry)
XX DE Amino acid sequence of a YggX homologue.
XX KW Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
XX KW hydroxyl radical; DNA damage; YggX homologue.
XX OS Klebsiella pneumoniae.
XX PN US2002072118-A1.
XX PD 13-JUN-2002.
XX PF 18-SEP-2001; 2001US-00955502.
XX PR 22-SEP-2000; 2000US-0234588P.
XX PA (DOWN/) DOWNS D.
XX PI (GRAL/) GRALNICK J A.
XX PI Downs D, Gralnick JA;
XX DR WPI; 2002-589476/63.
XX PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
XX PT cell, comprises engineering the cell to produce more YggX protein, a
XX PT protein identified from Salmonella enterica Serovar Typhimurium.
XX PS Example; Fig 1A; 16pp; English.
XX CC The specification describes a method for reducing superoxide damage to a
XX CC cell. The method comprises engineering the cell to produce more than the
XX CC native amount of YggX protein (a protein identified from Salmonella
XX CC enterica serovar typhimurium) or its homolog, where the cells are
XX CC rendered more resistant to superoxide damage. YggX reduces the oxidation
XX CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
XX CC clusters. The resulting decrease in free-iron levels generates fewer
XX CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
XX CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
XX CC cell. ABB78147-78 represent YggX homologues
XX SQ Sequence 78 AA;
    Query Match 81.3%; Score 395; DB 5; Length 78;
    Best Local Similarity 94.9%; Pred. No. 1e-37;
    Matches 74; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 MSRTTCTFLQREAGQDFQLYPGELGKRIYNEISKEAWAQWQHKTMLINEKLLMMNA 60
DB 1 MSRTTCTFLQREAGQDFQLYPGELGKRIYNEISKEAWAQWQHKTMLINEKLLMMNP 60
QY 61 EHRKLEQEMVNFLEFGK 78
DB 61 EHRKLEQEMVQFLFEKG 78
RESULT 14
ADF05158
ID ADF05158 standard; protein; 93 AA.
XX AC ADF05158;
XX AC ADF05158;
XX DT 12-FEB-2004 (first entry)
XX DE Bacterial polypeptide #1271.
XX KW Proteus mirabilis infection; bacterial infection; antibacterial;
XX KW immunostimulant.
XX OS Proteus mirabilis.
XX PR 22-SEP-2000; 2000US-0234588P.
XX PA (DOWN/) DOWNS D.
XX PN US6605709-B1.
XX PD 12-AUG-2003.
XX PF 05-APR-2000; 2000US-00543681.
XX PR 09-APR-1999; 99US-0128706P.
XX PA (GENO-) GENOME THERAPEUTICS CORP.
XX PI Breton GL;
XX DR WPI; 2003-895291/82.
XX DR N-PSDB; ADF00986.
XX PT New Proteus mirabilis polypeptides and polynucleotides, useful as
XX PT reagents for diagnosis of bacterial disease, as components of
XX PT antibacterial vaccines, as targets for antibacterial drugs, or as
XX PT biocontrol agents for plants.
XX PS Disclosure; SEQ ID NO 5443; 870pp; English.
XX CC The invention relates to new Proteus mirabilis polypeptides and...
XX CC polynucleotides. The invention also relates to antibodies against the
XX CC polypeptides, methods for producing the polypeptides, a method of
XX CC generating vaccines for immunising an individual against P. mirabilis, a
XX CC method for evaluating a compound for the ability to bind a P. mirabilis
XX CC polypeptide and a method for screening test compounds for anti-bacterial
XX CC activity. The polypeptides and polynucleotides are useful as molecular
XX CC targets for diagnosing, preventing and treating pathological conditions
XX CC resulting from bacterial infection, as reagents for diagnosis of
XX CC bacterial diseases, as components of antibacterial vaccines, as targets
XX CC for antibacterial drugs or as bio-control agents for plants. This
XX CC sequence represents a Proteus mirabilis polypeptide of the invention.
XX SQ Sequence 93 AA;
    Query Match 80.0%; Score 389; DB 7; Length 93;
    Best Local Similarity 80.0%; Pred. No. 6.1e-37;
    Matches 72; Conservative 7; Mismatches 11; Indels 0; Gaps 0;
QY 1 MSRTTCTFLQREAGQDFQLYPGELGKRIYNEISKEAWAQWQHKTMLINEKLLMMNA 60
DB 4 MSRTTCTFLNKEADGLDFQLYPGELGKRIYNEISKEAWAQWQHKTMLINEKLLMMNP 63
QY 61 EHRKLEQEMVNFLEFGKVEVHIEGYTPEDK 90
DB 64 DDKLLEQEMVRFLEFGHDVHIDGYTPPEK 93
RESULT 15
ABB78150
ID ABB78150 standard; protein; 91 AA.
XX AC ABB78150;
XX DT 05-NOV-2002 (first entry)
XX DE Amino acid sequence of a YggX homologue.
XX KW Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
XX KW hydroxyl radical; DNA damage; YggX homologue.
XX OS Unidentified.
XX PN US2002072118-A1.
XX PD 13-JUN-2002.
XX PF 18-SEP-2001; 2001US-00955502.
XX PR 22-SEP-2000; 2000US-0234588P.
XX PA (DOWN/) DOWNS D.

```


DR WPI; 2002-589476/63.

XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant

PT cell, comprises engineering the cell to produce more YggX protein, a

PT protein identified from *Salmonella enterica* Serovar Typhimurium.

XX Example; Fig 1A; 16pp; English.

XX

CC The specification describes a method for reducing superoxide damage to a

CC cell. The method comprises engineering the cell to produce more than the

CC native amount of YggX protein (a protein identified from *Salmonella*

CC enterica serovar typhimurium) or its homolog, where the cells are

CC rendered more resistant to superoxide damage. YggX reduces the oxidation

CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from

CC clusters. The resulting decrease in free-iron levels generates fewer

CC hydroxyl radicals and thus reduced DNA damage. The method is useful for

CC reducing superoxide damage in a bacterial, yeast, mammalian or plant

CC cell. ABB78147-78 represent YggX homologues

XX

XX Sequence 87 AA;

Query Match 52.5%; Score 255; DB 5; Length 87;

Best Local Similarity 55.2%; Pred. No. 1.9e-21;

Matches 48; Conservative 13; Mismatches 26; Indels 0; Gaps 0;

QY 1 MERTICTFLOREAGQDFQLYPGELGKRIYNEISKEAWAQHQTMLINEKKLMMNA 60

DB 1 MSRIIVNCVKLKEAEGLDPPYPGELGTRIQWQISKEAWEWQKIQTRLVNENRLNLADA 60

QY 61 EHRKLLQEQMNVNLFEGKEVHIEGYTP 87

DB 61 RARKYLQOQMERFLFEDGTVEAQGYVP 87

RESULT 23

ABB78149

ID ABB78149 standard; protein; 86 AA.

AC ABB78149;

XX

DT 05-NOV-2002 (first entry)

XX

DE Amino acid sequence of a YggX homologue.

XX

XX Superoxide damage; cell; YggX; *Salmonella enterica* serovar typhimurium;

KW hydroxyl radical; DNA damage; YggX homologue.

XX

OS Bordetella bronchiseptica.

XX

PN US2002072118-A1.

PN

PD 13-JUN-2002.

XX

PF 18-SEP-2001; 2001US-00955502.

XX

PR 22-SEP-2000; 2000US-0234588P.

XX

XX (DOWN/) DOWNS D.

PA (GRAL/) GRALNICK J A.

XX

XX Downs D, Gralnack JA;

PI

XX WPI; 2002-589476/63.

DR

XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant

PT cell, comprises engineering the cell to produce more YggX protein, a

PT protein identified from *Salmonella enterica* Serovar Typhimurium.

XX

XX Example; Fig 1A; 16pp; English.

PS

XX The specification describes a method for reducing superoxide damage to a

CC cell. The method comprises engineering the cell to produce more than the

CC native amount of YggX protein (a protein identified from *Salmonella*

CC enterica serovar typhimurium) or its homolog, where the cells are

CC rendered more resistant to superoxide damage. YggX reduces the oxidation

CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from

CC clusters. The resulting decrease in free-iron levels generates fewer

CC hydroxyl radicals and thus reduced DNA damage. The method is useful for

CC reducing superoxide damage in a bacterial, yeast, mammalian or plant

CC cell. ABB78147-78 represent YggX homologues

XX

XX Sequence 86 AA;

Query Match 49.6%; Score 241; DB 5; Length 86;

Best Local Similarity 54.8%; Pred. No. 7.7e-20;

Matches 46; Conservative 13; Mismatches 25; Indels 0; Gaps 0;

QY 1 MERTICTFLOREAGQDFQLYPGELGKRIYNEISKEAWAQHQTMLINEKKLMMNA 60

DB 1 MSRIIVNCVKLKEAEGLDPPYPGELGTRIQWQISKEAWEWQKIQTRLVNENRLNLADA 60

QY 61 EHRKLLQEQMNVNLFEGKEVHIEG 84

DB 61 RARKYLQOQMERFLFEDGTVEAQG 84

RESULT 24

ABB41576

ID AEB41576 standard; protein; 89 AA.

XX

AC AEB41576;

XX

DT 08-SEP-2005 (first entry)

XX

DE L. pneumophila protein SEQ ID NO 5908.

XX

KW detection; infection; Antibacterial; Vaccine.

XX

OS Legionella pneumophila.

XX

PN WO2005049642-A2.

PN

PD 02-JUN-2005.

XX

PF 23-SEP-2004; 2004WO-IB003578.

XX

PR 21-NOV-2003; 2003FR-00013687.

XX

PA (INSP) INST PASTEUR.

PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.

PA (UYLY-) UNIV LYON 1 BERNARD CLAUDE.

PA (CNRS) CNRS CENT NAT RECH SCI.

XX

PI Buchrieser C, Tichit M, Etienne J, Ma L, Cazalet C, Glaser P;

PI Rusniok C, Bouchier C, Zidane N, Magnier A, Kunst F, Vandenesch F;

PI Jarraud S;

XX

DR WPI; 2005-388305/40.

XX

XX New genome of *Legionella pneumophila* Paris strain and derived

PT polypeptides, useful for detection or identification of the strain and

PT for treatment and prevention of infections.

XX

XX Claim 3; SEQ ID NO 5908; 660pp; English.

XX

XX The invention relates to an isolated or purified nucleotide sequences (I)

CC from *Legionella pneumophila* Paris strain. (I), and their related

CC sequences or fragments, are useful as primers and probes for detection

CC and amplification, including differentiation between the Paris and

CC Philadelphia strains of *Legionella pneumophila* and to prepare recombinant

CC (hybrid) polypeptides (II). (II) are also useful for preparation of

CC specific antibodies (Ab), also used for detection/identification of

CC *Legionella*, and some (I), specifically those involved in synthesis of

CC surface proteins, are targets for identification of inhibitors. (II), or

CC vectors that contain (I), are useful as vaccines and immunogenic

CC compositions, for treatment and prevention of infections by L.

CC pneumophila. The present sequence represents the amino acid sequence of a
CC L. pneumophila protein.
XX
SQ Sequence 89 AA;

Query Match 47.6%; Score 231.5; DB 9; Length 89;
Best Local Similarity 53.8%; Pred. No. 1e-18;
Matches 43; Conservative 17; Mismatches 19; Indels 1; Gaps 1;
QY 1 MSRTTCTFLQRAEGQDFQYPGELGKRIYNEISKEAWQOHKQTMLINEKKNMNA 60
DB 1 MSRTVFCCCKLQEAEGLEKQFPFGEIGKVFNEVSKQANNMWSLHQTMLINEYRLNLIEA 60
QY 61 EHRKLEQEMVNFLE-EGKE 79
DB 61 RAREFLKEEMQKYFFGEGSE 80

RESULT 25
AEB38294
ID AEB38294 standard; protein; 95 AA.
XX
AC AEB38294;
XX
DT 08-SEP-2005 (first entry)
XX
DE L. pneumophila protein SEQ ID NO 2626.
XX
KW detection; infection; Antibacterial; Vaccine.
XX
OS Legionella pneumophila.
XX
PN WO2005049642-A2.
XX
PD 02-JUN-2005.
XX
PF 23-SEP-2004; 2004WO-IB003578.
XX
PR 21-NOV-2003; 2003PR-00013687.
XX
PA (INSP) INST PASTEUR.
XX
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
XX
PA (UPLY-) UNIV LYON 1 BERNARD CLAUDE.
XX
PA (CNRS) CNRS CENT NAT RECH SCI.
XX
PI Buchrieser C, Tichit M, Etienne J, Ma L, Cazalet C, Glaser P;
PI Rusniok C, Bouchier C, Zidane N, Magnier A, Kunst P, Vandenesch F;
PI Jarraud S;
XX
DR WPI; 2005-388305/40.

XX
XX New genome of Legionella pneumophila Paris strain and derived
PT polypeptides, useful for detection or identification of the strain and
PT for treatment and prevention of infections.
XX
PS Claim 3; SEQ ID NO 2626; 660pp; English.
XX
XX The invention relates to an isolated or purified nucleotide sequences (I)
CC from Legionella pneumophila Paris strain (I), and their related
CC sequences or fragments, are useful as primers and probes for detection
CC and amplification, including differentiation between the Paris and
CC Philadelphia strains of Legionella pneumophila and to prepare recombinant
CC (hybrid) polypeptides (II). (II) are also useful for preparation of
CC specific antibodies (Ab), also used for detection/identification of
CC Legionella, and some (I), specifically those involved in synthesis of
CC surface proteins, are targets for identification of inhibitors. (II), or
CC vectors that contain (I), are useful as vaccines and immunogenic
CC compositions, for treatment and prevention of infections by L.
CC pneumophila. The present sequence represents the amino acid sequence of a
XX L. pneumophila protein.
XX
SQ Sequence 95 AA;

Query Match 47.6%; Score 231.5; DB 9; Length 95;
Best Local Similarity 53.8%; Pred. No. 1e-18;
Matches 43; Conservative 17; Mismatches 19; Indels 1; Gaps 1;
QY 1 MSRTTCTFLQRAEGQDFQYPGELGKRIYNEISKEAWQOHKQTMLINEKKNMNA 60
DB 7 MSRTVFCCCKLQEAEGLEKQFPFGEIGKVFNEVSKQANNMWSLHQTMLINEYRLNLIEA 66
QY 61 EHRKLEQEMVNFLE-EGKE 79
DB 67 RAREFLKEEMQKYFFGEGSE 86
Search completed: June 27, 2007, 11:04:47
Job time : 219 secs

GenCore version 6.2.1
Copyright (c) 1993 - 2007 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: June 27, 2007, 11:01:26 ; Search time 347 Seconds
(without alignments)
281.162 Million cell updates/sec

Title: US-09-955-502A-11
Perfect score: 486
Sequence: 1 MSRTIFCTFLQREAGQDFQ.....NFLPEGKEVHIEGYTPDKK 91

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 3281787 seqs, 1072124677 residues

Total number of hits satisfying chosen parameters: 3281787

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 75 summaries

Database : UniProt_8.4.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	486	100.0	91	1 FETP_SHIBS	Q31wm4 shigella bo
2	486	100.0	91	1 FETP_SHIDS	Q32c31 shigella dy
3	486	100.0	91	1 FETP_SHISS	Q3yxe9 shigella so
4	486	100.0	91	2 Q1R763_ECOUT	Q1r763 escherichia
5	481	99.0	90	1 FETP_ECO57	P0a8p4 escherichia
6	481	99.0	90	1 FETP_ECOLI	P0a8p3 escherichia
7	481	99.0	90	1 FETP_SHIFL	P0a8p5 shigella fl
8	477	98.1	90	1 FETP_ECOL6	Q8fe19 escherichia
9	464	95.5	90	1 FETP_SALCH	Q57k04 salmonella
10	464	95.5	90	1 FETP_SALPA	Q5puml salmonella
11	464	95.5	90	1 FETP_SALTI	P67618 salmonella
12	464	95.5	90	1 FETP_SALTY	P67617 salmonella
13	411	84.6	90	1 FETP_ERWCT	Q6d8j9 erwinita car
14	404	83.1	90	1 FETP_ERPES	Q666m3 versinia ps
15	402	82.7	90	1 FETP_VIBCH	Q9kur4 vibrio chol
16	402	82.7	90	1 FETP_VIBVU	Q8dc55 vibrio vuln
17	402	82.7	90	1 FETP_VIBVY	Q7dmh14 vibrio vuln
18	399	82.1	90	1 FETP_VIBPA	Q81v15 vibrio para
19	397	81.7	90	2 Q1V3X2_VIBAL	Q1v3x2 vibrio algi
20	396	81.5	90	1 FETP_YERPE	Q8zhe7 versinia pe
21	396	81.5	90	2 Q1CEV2_YERPE	Q1cev2 versinia pe
22	396	81.5	90	2 Q1CB93_YERPE	Q1cb93 versinia pe
23	390	80.2	90	1 FETP_SODGM	Q2nr44 sodalis glo
24	389	80.0	91	1 FETP_MANSM	Q2nr47 mannheimia
25	387	79.6	90	1 FETP_HAE18	Q4gmd9 haemophilus
26	387	79.6	90	1 FETP_HAE19	P44048 haemophilus
27	382	78.6	90	1 FETP_PHOPR	Q61mk7 photobacter
28	382	78.6	90	2 Q1Z4G3_PHOPR	Q1z4g3 photobacter
29	381	78.4	90	1 FETP_PHOLL	Q7n711 photorhabd
30	379	78.0	90	1 FETP_PASMU	Q9clb9 pasteurella
31	374	77.0	90	2 Q12NG9_9VIBR	Q12ng9 vibrio angu

32	373	76.7	94	1 FETP_HAEDU	Q7vkb6 haemophilus
33	371	76.3	90	2 Q2C3L2_9GAMM	Q2c3l2 photobacter
34	366	75.3	90	1 FETP_VIBF1	Q5e7f0 vibrio fisc
35	363	74.7	90	1 FETP_PSEHT	Q3il19 pseudoalter
36	351	72.2	91	2 Q3QJD7_9GAMM	Q3qjd7 shewanella
37	343	70.6	92	2 Q33Q73_9GAMM	Q33q73 shewanella
38	342	70.4	92	2 Q2ZK9_SHEPU	Q2zrk9 shewanella
39	342	70.4	92	2 Q3Q7K0_9GAMM	Q3q7k0 shewanella
40	340	70.0	91	2 Q3P4C9_9GAMM	Q2x4m4 shewanella
41	339	69.8	92	2 Q2X4M4_9GAMM	Q2x4m4 shewanella
42	338	69.5	92	2 Q2Z5M5_9GAMM	Q2z5m5 shewanella
43	338	69.5	92	2 Q368P1_9GAMM	Q368p1 shewanella
44	335	68.9	90	1 FETP_IDILO	Q5qy58 idiomarina
45	335	68.9	92	2 Q3NNE3_SHEPR	Q3nne3 shewanella
46	332	68.3	92	1 FETP_SHEON	Q8ebx6 shewanella
47	326	67.1	89	2 Q1FVU6_9GAMM	Q1fwu6 psychromona
48	324	66.7	90	1 FETP_COLP3	Q47wl9 colwellia p
49	318	65.4	90	2 Q1SZT1_ALTAT	Q1sztl pseudoalter
50	316	65.0	89	2 Q1ZS28_BAUCH	Q1zsf27 psychromona
51	283	58.2	77	2 Q1LSZ8_BAUCH	Q1lsz8 baumannia c
52	265	54.5	77	1 FETP_BUCAI	P57618 buchnera ap
53	255	52.5	90	1 FETP_BORAI	Q2kyq6 bordetella
54	255	52.5	90	1 FETP_BORBR	Q7wh06 bordetella
55	255	52.5	90	1 FETP_BORPA	Q7w942 bordetella
56	255	52.5	90	1 FETP_BORPE	Q7wvc4 bordetella
57	247	50.8	78	1 FETP_BUCAP	Q8k925 buchnera ap
58	239	49.2	90	1 FETP_NITOC	Q3j8x0 nitrosococc
59	237	48.9	84	1 FETP_BLOPB	Q493f6 blochmannia
60	237	48.8	90	1 FETP_DECAR	Q47al9 dechloromon
61	235	48.4	78	1 FETP_WIGBR	Q8d3c5 wiggleswort
62	233	47.9	90	1 FETP_RHOFO	Q21wm7 rhodofera
63	231	47.6	89	1 FETP_LEGPA	Q5x3x9 legionella
64	231	47.6	89	1 FETP_LEGPH	Q5zu80 legionella
65	231	47.5	90	1 FETP_PSEAE	Q9hu36 pseudomonas
66	231	47.5	91	1 FETP_XANAC	Q9pj17 xanthomonas
67	230	47.3	109	2 Q1HS33_METPL	Q1hs33 methylobaci
68	229	47.1	91	1 FETP_XANCS	Q3brx9 xanthomonas
69	228	47.0	89	1 FETP_LEGPL	Q5wvc4 legionella
70	227	46.7	90	1 FETP_COXBU	Q83d06 coxiella bu
71	227	46.7	90	1 FETP_PSE14	Q48c72 pseudomonas
72	227	46.7	90	1 FETP_PSESM	Q87u53 pseudomonas
73	227	46.7	90	1 FETP_PSEU2	Q9pc73 pseudomonas
74	226	46.5	90	1 FETP_XYLFA	Q98r49 xylella fas
75	225	46.3	90	1 FETP_PSEPK	Q98r49 pseudomonas

ALIGNMENTS

RESULT 1
FETP_SHIBS
ID FETP_SHIBS STANDARD; PRT; 91 AA.
AC Q31WM4;
DT 11-JUL-2006, integrated into UniProtKB/Swiss-Prot.
DT 06-DEC-2005, sequence version 1.
DT 11-JUL-2006, entry version 7.
DE Probable Pe(2+)-trafficking protein.
GN Name-ygsX; OrderedLocusNames=S803028;
OS Shigella boydii serotype 4 (strain Sb227).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Shigella.
OX NCBI_TaxID=300268;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=16275786; DOI=10.1093/nar/gki1954;
RA Yang F., Yang J., Zhang X., Chen L., Jiang Y., Yan Y., Tang X.,
Wang J., Xiong Z., Dong J., Xue Y., Xu X., Sun L., Chen S.,
Nie H., Peng J., Xu J., Wang Y., Yuan Z., Wen Y., Yao Z., Shen Y.,
Qiang B., Hou Y., Yu J., Jin Q.;
RT "Genome dynamics and diversity of Shigella species, the etiologic agents of bacillary dysentery.";
RL Nucleic Acids Res. 33:6445-6458(2005).
CC -!- FUNCTION: Could be a mediator in iron transactions between iron

CC acquisition and iron-requiring processes, such as synthesis and/or
 CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
 CC -!- SUBUNIT: Monomer (By similarity).
 CC -!- SIMILARITY: Belongs to the Fe(2+)-trafficking protein family.
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 DR EMBL: CP000036; ABB67534.1; -; Genomic_DNA.
 DR SMR: Q31WM4; 1-91.
 DR GenomeReviews: CP000036_GR; SBO_3028.
 DR HAMAP: MF_00686; -; 1.
 DR InterPro: IPR007457; YggX.
 DR Pfam: PF04362; Iron_traffic; 1.
 DR PIRSF: PIRSF029827; Fe_traffic_YggX; 1.
 DR ProDom: PD029191; DUF495; 1.
 KW Complete proteome; Iron.
 FT CHAIN 1
 FT PROBABLY Fe(2+)-trafficking protein.
 FT FTID=PRO_0000246116.
 SQ SEQUENCE 91 AA; 10953 MW; 1E3625B77C32B94B CRC64;
 Query Match 100.0%; Score 486; DB 1; Length 91;
 Best Local Similarity 100.0%; Pred. No. 7.3e-42;
 Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSRTICTFLQREAGQDFQLYPGLGKRIYNEISKEAWAQWQHKTMLINEKLLNMNNA 60
 DB 1 MSRTICTFLQREAGQDFQLYPGLGKRIYNEISKEAWAQWQHKTMLINEKLLNMNNA 60
 QY 61 EHRKLEQEMVNFLEPGKEVHIEGYTPEDKK 91
 DB 61 EHRKLEQEMVNFLEPGKEVHIEGYTPEDKK 91
 RESULT 3
 FETP_SHISS STANDARD; PRT; 91 AA.
 AC Q3YXE9;
 DT 11-JUL-2006, integrated into UniProtKB/Swiss-Prot.
 DT 27-SEP-2005, sequence version 1.
 DE Probable Fe(2+)-trafficking protein.
 GN Name=YggX; OrderedLocusNames=SSO_3234;
 OS Shigella sonnei (strain Ss046).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Shigella.
 OX NCBI_TaxID=300269;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RX PubMed:16275786; DOI=10.1093/nar/gki954;
 RA Yang F., Yang J., Zhang X., Chen L., Jiang Y., Yan Y., Tang X.,
 RA Wang J., Xiong Z., Dong J., Xue Y., Zhu Y., Xu X., Sun L., Chen S.,
 RA Nie H., Peng J., Xu J., Wang Y., Yuan Z., Wen Y., Yao Z., Shen Y.,
 RA Qiang B., Hou Y., Yu J., Jin Q.;
 RT "Genome dynamics and diversity of Shigella species, the etiologic
 RT agents of bacillary dysentery".
 RL Nucleic Acids Res. 33:6445-6458(2005).
 CC -!- FUNCTION: Could be a mediator in iron transactions between iron
 CC acquisition and iron-requiring processes, such as synthesis and/or
 CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
 CC -!- SUBUNIT: Monomer (By similarity).
 CC -!- SIMILARITY: Belongs to the Fe(2+)-trafficking protein family.
 CC -----
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 CC -----
 DR EMBL: CP000038; AAZ89813.1; -; Genomic_DNA.
 DR SMR: Q3YXE9; 1-91.
 DR GenomeReviews: CP000038_GR; SSO_3234.
 DR HAMAP: MF_00686; -; 1.
 DR InterPro: IPR007457; YggX.
 DR Pfam: PF04362; Iron_traffic; 1.
 DR PIRSF: PIRSF029827; Fe_traffic_YggX; 1.
 DR ProDom: PD029191; DUF495; 1.
 KW Complete proteome; Iron.
 FT CHAIN 1
 FT PROBABLY Fe(2+)-trafficking protein.
 FT FTID=PRO_0000246118.
 SQ SEQUENCE 91 AA; 10953 MW; 1E3625B77C32B94B CRC64;
 Query Match 100.0%; Score 486; DB 1; Length 91;
 Best Local Similarity 100.0%; Pred. No. 7.3e-42;
 Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSRTICTFLQREAGQDFQLYPGLGKRIYNEISKEAWAQWQHKTMLINEKLLNMNNA 60
 DB 1 MSRTICTFLQREAGQDFQLYPGLGKRIYNEISKEAWAQWQHKTMLINEKLLNMNNA 60
 QY 61 EHRKLEQEMVNFLEPGKEVHIEGYTPEDKK 91

RESULT 2

FETP_SHISS STANDARD; PRT; 91 AA.
 AC Q32C31;
 DT 11-JUL-2006, integrated into UniProtKB/Swiss-Prot.
 DT 06-DEC-2005, sequence version 1.
 DE Probable Fe(2+)-trafficking protein.
 GN Name=YggX; OrderedLocusNames=SDY_3110;
 OS Shigella dysenteriae serotype 1 (strain Sd197).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Shigella.
 OX NCBI_TaxID=300267;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RX PubMed:16275786; DOI=10.1093/nar/gki954;
 RA Yang F., Yang J., Zhang X., Chen L., Jiang Y., Yan Y., Tang X.,
 RA Wang J., Xiong Z., Dong J., Xue Y., Zhu Y., Xu X., Sun L., Chen S.,
 RA Nie H., Peng J., Xu J., Wang Y., Yuan Z., Wen Y., Yao Z., Shen Y.,
 RA Qiang B., Hou Y., Yu J., Jin Q.;
 RT "Genome dynamics and diversity of Shigella species, the etiologic
 RT agents of bacillary dysentery".
 RL Nucleic Acids Res. 33:6445-6458(2005).
 CC -!- FUNCTION: Could be a mediator in iron transactions between iron
 CC acquisition and iron-requiring processes, such as synthesis and/or
 CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
 CC -!- SUBUNIT: Monomer (By similarity).
 CC -!- SIMILARITY: Belongs to the Fe(2+)-trafficking protein family.
 CC -----
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 CC -----
 DR EMBL: CP000034; ABB63124.1; -; Genomic_DNA.
 DR SMR: Q32C31; 1-91.
 DR GenomeReviews: CP000034_GR; SDY_3110.
 DR HAMAP: MF_00686; -; 1.
 DR InterPro: IPR007457; YggX.
 DR Pfam: PF04362; Iron_traffic; 1.
 DR PIRSF: PIRSF029827; Fe_traffic_YggX; 1.

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Postal G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grobeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamouis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blatner F.R.;
"genome sequence of enterohaemorrhagic Escherichia coli O157:H7";
Nature 409:529-533(2001).
[2]
NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
STRAN=O157:H7 / Sakai / RIMD 0509952 / EHEC;
MEDLINE=21156231; PubMed=11258796; DOI=10.1093/dnares/8.1.11;
Hayashi T., Makino K., Onishi M., Kurokawa K., Ishii K., Yokoyama K.,
Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
Kuhara S., Shiba T., Hattori M., Shinagawa H.;
"Complete genome sequence of enterohaemorrhagic Escherichia coli
O157:H7 and genomic comparison with a laboratory strain K-12";
DNA Res. 8:11-22(2001).
CC -1- FUNCTION: Could be a mediator in iron transactions between iron
acquisition and iron-requiring processes, such as synthesis and/or
repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- SIMILARITY: Belongs to the Fe(2+)-trafficking protein family.

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EMBL: AB005174; AAC58093.1; -; Genomic_DNA.
ENBL: BA000007; BAB37261.1; -; Genomic_DNA.
DR PIR: A85954; A85954.
DR PIR: F91108; F91108.
DR SNR: POA8P4; 1-90.
DR GenomeReviews: BA000007 GR; RCS3838.
DR GenomeReviews: AE005174 GR; Z4307.
DR HAMAP: MF_00686; -, 1
DR InterPro: IPR007457; YggX.
DR Pfam: PF04362; Iron traffic; 1.
DR PRSF: PRSF029827; Fe traffic_YggX; 1.
DR ProDom: PD029191; DUF495; 1.
KW Complete proteome; Iron.
FT INIT MET 0 0
FT CHAIN 1 90
FT FT
SQ SEQUENCE 90 AA; 10821 MW; D7C66C2A35E62402 CRC64;
Query Match 99.0%; Score 481; DB 1; Length 90;
Best Local Similarity 100.0%; Pred. No. 2.3e-41;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0
QY 2 SRTIFCTFLQREAGQDFOLYPGELGKRIYNEISKEAWAQHQKOTMLINEKLNMMNAE 61
DB 1 SRTIFCTFLQREAGQDFOLYPGELGKRIYNEISKEAWAQHQKOTMLINEKLNMMNAE 60
QY 62 HRKLLQEMVNFLEFGKEVHIEGYTPEDKK 91
DB 61 HRKLLQEMVNFLEFGKEVHIEGYTPEDKK 90
RESULT 6
FETP_ECOLI STANDARD; PRT; 90 AA.
AC POA8P3; P52065; Q2M9N1.
DT 07-JUN-2005, integrated into UniProtKB/Swiss-Prot.
DT 07-JUN-2005, sequence version 1.
DT 11-JUL-2006, entry version 12.
DE Probable Fe(2+)-trafficking protein.
OS Names=YggX; OrderedLocusNames=b2962;
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
NCBI_TaxID=562;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RC STRAIN=K12 / MG1655 / ATCC 47076;
RX MEDLINE=97426617; PubMed=9278503; DOI=10.1126/science.277.5331.1453;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.,
RA "The complete genome sequence of *Escherichia coli* K-12.";
RL Science 277:1453-1474(1997).
RN [2]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RN STRAIN=K12 / W3110 / ATCC 27325 / DSM 5911,
RC DOI=10.1038/nmbo4100049;
RX Hayashi K., Morooka N., Yamamoto Y., Fujita K., Isono K., Choi S.,
RA Ohtsubo E., Baba T., Wanner B.L., Mori H., Horiuchi T.;
RA "Highly accurate genome sequences of *Escherichia coli* K-12 strains
MG1655 and W3110.";
RL Mol. Syst. Biol. 2:E1-E5(2006).
RN [3]
RN PARTIAL PROTEIN SEQUENCE OF 1-12.
RC STRAIN=K12 / EMG2;
RX MEDLINE=97443975; PubMed=9298646;
RA Link A.J., Robison K., Church G.M.;
RT "Comparing the predicted and observed properties of proteins encoded
in the genome of *Escherichia coli* K-12.";
RL Electrophoresis 18:1259-1313(1997).
RN [4]
RN PROTEIN SEQUENCE OF 1-10.
RC STRAIN=K12;
RX MEDLINE=99085675; PubMed=9868784;
RA Wasinger V.C., Humphrey-Smith I.;
RT "Small genes/gene-products in *Escherichia coli* K-12.";
RL FEMS Microbiol. Lett. 169:375-382(1998).
RN [5]
RN IDENTIFICATION BY MASS SPECTROMETRY.
RC MEDLINE=99420866; PubMed=10493123;
RX DOI=10.1002/ISICI.1522-2683(19990801)20:11<2181::AID-ELPS2181>3.3.CO;2-H;
RA Fountoulakis M., Takacs M.-F., Berndt P., Langen H., Takacs B.;
RT "Enrichment of low abundance proteins of *Escherichia coli* by
hydroxyapatite chromatography.";
RL Electrophoresis 20:2181-2195(1999).
RN [6]
RN INDUCTION, AND FUNCTION.
RC STRAIN=K12 / GC4468;
RX PubMed=14594836; DOI=10.1128/JB.185.22.6624-6632.2003;
RA Pomposiello P.J., Koutsoloutsou A., Carrasco D., Dempfle B.;
RT "SoxRS-regulated expression and genetic analysis of the *ygxB* gene of
Escherichia coli.";
RL J. Bacteriol. 185:6624-6632(2003).
RN [7]
RN STRUCTURE BY NMR, AND FUNCTION.
RC PubMed=15983188; DOI=10.1110/ps.051358105;
RA Osborne M.J., Siddiqui N., Landgraf D., Pomposiello P.J., Gehring K.;
RT "The solution structure of the oxidative stress-related protein YggX
from *Escherichia coli*.";
RL Protein Sci. 14:1673-1678(2005).
RN CC -!- FUNCTION: Could be a mediator in iron transactions between iron
acquisition and iron-requiring processes, such as synthesis and/or
repair of Fe-S clusters in biosynthetic enzymes. Necessary to
maintain high levels of aconitase under oxidative stress.
RN CC -!- SUBUNIT: Monomer (Probable).
RN CC -!- INDUCTION: By oxidative stress and soxS.
RN CC -!- SIMILARITY: Belongs to the Fe(2+)-trafficking protein family.
RN CC
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RN -----
RN EMBL; U28377; AAA69129.1; -; Genomic DNA.
RN EMBL; U00096; AAC75999.1; -; Genomic DNA.
RN EMBL; AP009048; BAE77025.1; -; Genomic_DNA.
RN PIR; A65082; A65082.
RN PDB; 1YHD; NMR; A=1-90.
RN SWISS-2DPAGE; P0A8P3; COLI.
RN GenomeReviews; U00096 GR; b2962.
RN DR

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RA Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S.,
RA Schwartz D.C., Blattner F.R.;
RT "Complete genome sequence and comparative genomics of Shigella
RL flexneri serotype 2a strain 2457T.";
RL Infect. Immun. 71:2775-2786(2003).
CC -!- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -!- SUBUNIT: Monomer (By similarity).
CC -!- SIMILARITY: Belongs to the Fe(2+)-trafficking protein family.
CC
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CC -----
DR EMBL; AB005674; AAN44440.1; -; Genomic DNA.
DR EMBL; AB014073; AAP18264.1; -; Genomic DNA.
DR SMR; POA8P5; 1-90.
DR GenomeReviews; AB014073 GR; S 3162.
DR GenomeReviews; AB005674 GR; SF2959.
DR HAMAP; MF_00686; -; 1.
DR InterPro; IPR007457; YggX.
DR Pfam; PF04362; Iron traffic; 1.
DR PIRSF; PIRSF029827; Fe traffic_YggX; 1.
DR ProDom; PD029191; DUF495; 1.
DR Complete proteome; Iron.
KW Complete proteome; Iron.
FT INIT MET 0 0 By similarity.
FT CHAIN 1 90 Probable Fe(2+)-trafficking protein.
FT FTID=PRO_0000214507.
FT SEQUENCE 90 AA; 10821 MW; D7C66C2A35E62402 CRC64;
Query Match 99.0%; Score 481; DB 1; Length 90;
Best Local Similarity 100.0%; Pred. No. 2.3e-41;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 SRTIFCTFLQREAGQDFQYLGELGKRIYNEISKEAWAQWQHKTMLINEKLNMMNAE 61
DB 1 SRTIFCTFLQREAGQDFQYLGELGKRIYNEISKEAWAQWQHKTMLINEKLNMMNAE 60
QY 62 HRKLEQEMVNFLEFGKEVHIEGYTPEDKK 91
DB 61 HRKLEQEMVNFLEFGKEVHIEGYTPEDKK 90
RESULT 8
FETP_ECOL6
ID FETP_ECOL6 STANDARD; PRT; 90 AA.
AC Q8FEI9;
DT 25-JUL-2003, integrated into UniProtKB/Swiss-Prot.
DT 25-JUL-2003, sequence version 2.
DT 11-JUL-2006, entry version 21.
DE Probable Fe(2+)-trafficking protein.
GN Name=YggX; OrderedLocNames=c_3550;
OS Escherichia coli O6.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=217992;
RN [1]_
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=06:HI / CFT073 / ATCC 700928 / UPSC;
RX MEDLINE=22388234; PubMed=12471157; DOI=10.1073/pnas.252529799;
RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
RA Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
RA Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
RA Mobley H.L.T., Domeneberg M.S., Blattner F.R.;
RT "Extensive mosaic structure revealed by the complete genome sequence
RL of uropathogenic Escherichia coli.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
CC -!- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -!- SUBUNIT: Monomer (By similarity).
CC -!- SIMILARITY: Belongs to the Fe(2+)-trafficking protein family.
CC -----
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CC -----
DR EMBL; AB014075; AAN81998.1; -; Genomic DNA.
DR SMR; Q8FEI9; 1-90.
DR GenomeReviews; AB014075 GR; c_3550.
DR BioCyc; ECOL199310:C3550-MONOMER; -.
DR HAMAP; MF_00686; -; 1.
DR InterPro; IPR007457; YggX.
DR Pfam; PF04362; Iron traffic; 1.
DR PIRSF; PIRSF029827; Fe traffic_YggX; 1.
DR ProDom; PD029191; DUF495; 1.
DR Complete proteome; Iron.
KW Complete proteome; Iron.
FT INIT MET 0 0 By similarity.
FT CHAIN 1 90 Probable Fe(2+)-trafficking protein.
FT FTID=PRO_0000214480.
FT SEQUENCE 90 AA; 10805 MW; D7C66C2A35E63692 CRC64;
Query Match 98.1%; Score 477; DB 1; Length 90;
Best Local Similarity 98.9%; Pred. No. 6e-41;
Matches 89; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 2 SRTIFCTFLQREAGQDFQYLGELGKRIYNEISKEAWAQWQHKTMLINEKLNMMNAE 61
DB 1 SRTIFCTFLQREAGQDFQYLGELGKRIYNEISKEAWAQWQHKTMLINEKLNMMNAE 60
QY 62 HRKLEQEMVNFLEFGKEVHIEGYTPEDKK 91
DB 61 HRKLEQEMVNFLEFGKEVHIEGYTPEDKK 90
RESULT 9
FETP_SALCH
ID FETP_SALCH STANDARD; PRT; 90 AA.
AC Q57K04;
DT 19-JUL-2005, integrated into UniProtKB/Swiss-Prot.
DT 19-JUL-2005, sequence version 2.
DT 11-JUL-2006, entry version 13.
DE Probable Fe(2+)-trafficking protein.
GN Name=YggX; OrderedLocNames=SCH_3052;
OS Salmonella choleraesuis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=591;
RN [1]_
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=SC-B67;
RX PubMed=15781495; DOI=10.1093/nar/gki297;
RA Chiu C.-H., Tang P., Chu C., Hu S., Bao Q., Yu J., Chou Y.-Y.,
RA Wang H.-S., Lee Y.-S.;
RT "The genome sequence of Salmonella enterica serovar Choleraesuis, a
RT highly invasive and resistant zoonotic pathogen.";
RL Nucleic Acids Res. 33:1690-1698(2005).
CC -!- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -!- SUBUNIT: Monomer (By similarity).
CC -!- SIMILARITY: Belongs to the Fe(2+)-trafficking protein family.
CC
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CC -----
DR EMBL; AB017220; AAX66958.1; -; Genomic DNA.
DR SMR; Q57K04; 1-90.
DR GenomeReviews; AB017220 GR; SCH_3052.
DR HAMAP; MF_00686; -; 1.
DR InterPro; IPR007457; YggX.
DR Pfam; PF04362; Iron traffic; 1.
DR ProDom; PD029191; DUF495; 1.
DR Complete proteome; Iron.
KW Complete proteome; Iron.
FT INIT MET 0 0 By similarity.
FT CHAIN 1 90 Probable Fe(2+)-trafficking protein.
FT FTID=PRO_0000214502.
FT
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SQ SEQUENCE 90 AA; 10768 MW; B3B6A1BE22555E3C CRC64;

Query Match 95.5%; Score 464; DB 1; Length 90;
 Best Local Similarity 94.4%; Pred. No. 1.3e-39;
 Matches 85; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 2 SRTIFCTFLQRAEGQDFQLYPGEIGKRYNEISKEAWAOWHOKOTMLINEKKNMNAE 61
 DB 1 SRTIFCTFLQRAEGQDFQLYPGEIGKRYNEISKEAWAOWHOKOTMLINEKKNMNAE 60

QY 62 HRKLEQEMVNFLEPGKEVHIEGYTPEDKK 91
 DB 61 HRKLEQEMVNFLEPGKDVHIEGYTPEDKK 90

RESULT 10
 FETP SALPA
 ID FETP SALPA STANDARD; PRT; 90 AA.
 AC QSPM1;
 DT 19-JUL-2005, integrated into UniProtKB/Swiss-Prot.
 DT 11-JUL-2006, entry version 11.
 DE Probable Fe(2+)-trafficking protein.
 GN Name-yggX; OrderedLocusNames=SPA2974;
 OS Salmonella paratyphi-a.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Salmonella.
 OX NCBI_TaxID=54388;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=ATCC 9150 / SARB42;
 RX PubMed=15531882; DOI=10.1038/ngl470;
 RA McClelland M., Sabo A., Meyer R., Bieri T., Ozersky P., McLellan M.,
 RA Porwollik S., Wang C., Nguyen C., Berghoff A., Elliott G.,
 RA Harkins C.R., Wang C., Carter J., Kremizki C., Layman D.,
 RA Kohlberg S., Strong C., Du F., Miner T., Minx P.,
 RA Leonard S., Sun H., Fulton L., Nish W., Miner T., Minx P.,
 RA Delehaanty K., Fronick C., Magrini V., Nhan M., Warren W., Florea L.,
 RA Spieth J., Wilson R.K.;
 RT "Comparison of genome degradation in Paratyphi A and Typhi, human-
 RT restricted serovars of Salmonella enterica that cause typhoid.";
 RL Nat. Genet. 36:1268-1274(2004).
 CC -!- FUNCTION: Could be a mediator in iron transactions between iron
 CC acquisition and iron-requiring processes, such as synthesis and/or
 CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
 CC -!- SUBUNIT: Monomer (By similarity).
 CC -!- SIMILARITY: Belongs to the Fe(2+)-trafficking protein family.
 CC
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 CC
 CC EMBL; CP000026; AAV78812.1; -; Genomic_DNA.
 CC SMR; QSPM1; 1-90.
 CC GenomeReviews; CP000026_GR; SPA2974.
 CC HAMAP; MF_00686; -; 1.
 CC InterPro; IPR007457; YggX.
 CC Pfam; PF04362; Iron traffic; 1.
 CC ProDom; PD029191; DUF495; 1.
 CC Complete proteome; Iron.
 KW Complete proteome; Iron.
 FT INIT MET 0 0 By similarity.
 FT CHAIN 1 90 Probable Fe(2+)-trafficking protein.
 FT /FTID=PRO_0000214503.
 SQ SEQUENCE 90 AA; 10768 MW; B3B6A1BE22555E3C CRC64;

Query Match 95.5%; Score 464; DB 1; Length 90;
 Best Local Similarity 94.4%; Pred. No. 1.3e-39;
 Matches 85; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 2 SRTIFCTFLQRAEGQDFQLYPGEIGKRYNEISKEAWAOWHOKOTMLINEKKNMNAE 61
 DB 1 SRTIFCTFLQRAEGQDFQLYPGEIGKRYNEISKEAWAOWHOKOTMLINEKKNMNAE 60

QY 62 HRKLEQEMVNFLEPGKEVHIEGYTPEDKK 91

DB 61 HRKLEQEMVNFLEPGKDVHIEGYTPEDKK 90

RESULT 11
 FETP SALTI
 ID FETP SALTI STANDARD; PRT; 90 AA.
 AC F67618; Q8AFV6;
 DT 11-OCT-2004, integrated into UniProtKB/Swiss-Prot.
 DT 11-OCT-2004, sequence version 1.
 DE Probable Fe(2+)-trafficking protein.
 DE Name-yggX; OrderedLocusNames=STY3266, t3024;
 GN Salmonella typhi.
 OS Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Salmonella.
 OX NCBI_TaxID=601;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=CT18;
 RX MEDLINE=21534947; PubMed=11677608; DOI=10.1038/35101607;
 RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
 RA Churcher C.M., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,
 RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
 RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
 RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
 RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
 RA Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K.,
 RA Whitehead S., Barrell B.G.;
 RT "Complete genome sequence of a multiple drug resistant Salmonella
 RT enterica serovar Typhi CT18.";
 RL Nature 413:848-852(2001).
 RN [2]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=ATCC 700931 / Ty2;
 RX MEDLINE=22531367; PubMed=12644504;
 RX DOI=10.1128/JB.185.7.2330-2337.2003;
 RA Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
 RA Burland V., Kodoyanni V., Schwartz D.C., Blattner F.R.;
 RT "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
 RT and CT18.";
 RL J. Bacteriol. 185:2330-2337(2003).
 CC -!- FUNCTION: Could be a mediator in iron transactions between iron
 CC acquisition and iron-requiring processes, such as synthesis and/or
 CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
 CC -!- SUBUNIT: Monomer (By similarity).
 CC -!- SIMILARITY: Belongs to the Fe(2+)-trafficking protein family.
 CC
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 CC
 CC EMBL; AL627277; CAD02936.1; -; Genomic_DNA.
 CC EMBL; AE014613; AAO70576.1; -; Genomic_DNA.
 CC SMR; P67618; 1-90.
 CC GenomeReviews; AL513382_GR; STY3266.
 CC HAMAP; MF_00686; -; 1.
 CC InterPro; IPR007457; YggX.
 CC Pfam; PF04362; Iron traffic; 1.
 CC PIRSF; PIRSF029827; Fe traffic; 1.
 CC ProDom; PD029191; DUF495; 1.
 CC Complete proteome; Iron.
 KW Complete proteome; Iron.
 FT INIT MET 0 0 By similarity.
 FT CHAIN 1 90 Probable Fe(2+)-trafficking protein.
 FT /FTID=PRO_0000214504.
 SQ SEQUENCE 90 AA; 10768 MW; B3B6A1BE22555E3C CRC64;

Query Match 95.5%; Score 464; DB 1; Length 90;
 Best Local Similarity 94.4%; Pred. No. 1.3e-39;
 Matches 85; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 2 SRTIFCTFLQRAEGQDFQLYPGEIGKRYNEISKEAWAOWHOKOTMLINEKKNMNAE 61
 DB 1 SRTIFCTFLQRAEGQDFQLYPGEIGKRYNEISKEAWAOWHOKOTMLINEKKNMNAE 61

QY 62 HRKLEQEMVNFLEPGKEVHIEGYTPEDKK 91

Db 1 SRTICTYLDRAEGDQFOLYPGELGKRIYNEISKDAWAQWQHKTMLINEKKNMNAE 60
QY 62 HRKLEQEMVNFLEGGKVEHIEGYTPEDKK 91
Db 61 HRKLEQEMVNFLEGGKVEHIEGYTPEDKK 90

RESULT 12
FETP_SALTY STANDARD; PRT; 90 AA.
AC P67617; Q8XPFV6;
DT 11-OCT-2004, integrated into UniProtKB/Swiss-Prot.
DT 11-OCT-2004, sequence version 1.
DT 11-JUL-2006, entry version 16.
DE Probable Fe(2+)-trafficking protein.
GN Name=yggX; OrderedLocusNames=STM3111;
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=602;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=LT2 / SGSC1412 / ATCC 700720;
RX MEDLINE=21534948; PubMed=11677609; DOI=10.1038/35101614;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali J., Dante M., Du P., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
LT2.";
RL Nature 413:852-856 (2001).
RN [2]
RP FUNCTION.
RC STRAIN=LT2;
RX PubMed=11416172; DOI=10.1073/pnas.151243198;
RA Gralnick J.A., Downs D.M.;
RT "Protection from superoxide damage associated with an increased level
of the YggX protein in Salmonella enterica.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:8030-8035 (2001).
RN [3]
RP FUNCTION, AND MUTAGENESIS OF CYS-6.
RC STRAIN=LT2;
RX PubMed=12670952; DOI=10.1074/jbc.M301577200;
RA Gralnick J.A., Downs D.M.;
RT "The YggX protein of Salmonella enterica is involved in Fe(II)
trafficking and minimizes the DNA damage caused by hydroxyl radicals:
residue Cys-7 is essential for yggX function.";
RL J. Biol. Chem. 278:20708-20715 (2003).
RN [4]
RP FUNCTION.
RC STRAIN=LT2;
RX PubMed=15516576; DOI=10.1128/JB.186.22.7626-7634.2004;
RA Skovran E., Laumon C.T., Downs D.M.;
RT "Lack of YggX results in chronic oxidative stress and uncovers subtle
defects in Fe-S cluster metabolism in Salmonella enterica.";
RL J. Bacteriol. 186:7626-7634 (2004).
CC 1- FUNCTION: Could be a mediator in iron transactions between iron
acquisition and iron-requiring processes, such as synthesis and/or
repair of Fe-S clusters in biosynthetic enzymes. Necessary to
maintain high levels of aconitase under oxidative stress.
CC 1- SIMILARITY: Belongs to the Fe(2+)-trafficking protein family.
CC
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CC EMBL: A3008843; RAL21986.1; -; Genomic_DNA.
CC PDB: 1X58; NMR: A=1-90.
CC GenomeReviews: AE006468_GR; STM3111.
CC StyGene; SG27777; YGGX.
CC HAMAP; MF_00686; -; 1.
CC InterPro; IPR007457; YggX.
CC Pfam; PF04362; Iron_traffic; 1.

DR PIRSF029827; Fe_traffic_YggX; 1.
DR ProDom; PD029191; DUF495; 1.
KW 3D-structure; Complete proteome; Iron.
FT INIT MET 0 By similarity.
FT CHAIN 1 90 Probable Fe(2+)-trafficking protein.
/FTid=PRO_0000214505.
FT MUTAGEN C6 6 C->S: Strong decrease in activity.
FT STRAND 3 5
FT TURN 7 9
FT STRAND 10 15
FT STRAND 20 21
FT STRAND 23 23
FT HELIX 24 30
FT TURN 31 32
FT STRAND 34 34
FT HELIX 35 52
FT TURN 56 57
FT STRAND 58 58
FT HELIX 59 73
FT TURN 74 74
FT STRAND 78 79
FT STRAND 83 84
FT STRAND 87 88
SQ SEQUENCE 90 AA; 10768 MW; B3B6A1EE22555E3C CRC64;
Query Match 95.5%; Score 464; DB 1; Length 90;
Best Local Similarity 94.4%; Pred. No. 1.3e-39;
Matches 85; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
QY 2 SRTICTYLDRAEGDQFOLYPGELGKRIYNEISKDAWAQWQHKTMLINEKKNMNAE 61
Db 1 SRTICTYLDRAEGDQFOLYPGELGKRIYNEISKDAWAQWQHKTMLINEKKNMNAE 60
QY 62 HRKLEQEMVNFLEGGKVEHIEGYTPEDKK 91
Db 61 HRKLEQEMVNFLEGGKVEHIEGYTPEDKK 90

RESULT 13
FETP_ERWCT STANDARD; PRT; 90 AA.
AC Q6D6J9;
DT 19-JUL-2005, integrated into UniProtKB/Swiss-Prot.
DT 16-AUG-2004, sequence version 1.
DT 11-JUL-2006, entry version 13.
DE Probable Fe(2+)-trafficking protein.
GN OrderedLocusNames=EC0975;
OS Erwinia carotovora subsp. atroseptica (Pectobacterium atrosepticum).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Pectobacterium.
OX NCBI_TaxID=29471;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=SCRI 1043 / ATCC BAA-672;
RX PubMed=15263089; DOI=10.1073/pnas.0402424101;
RA Bell K.S., Sebaiha M., Pritchard L., Holden M.T.G., Hyman L.J.,
RA Holeva M.C., Thomson N.R., Bentley S.D., Church L.J.C., Mungall K.,
RA Atkin R., Bason N., Brooks K., Chillingworth T., Clark K., Doggett J.,
RA Fraser A., Hance Z., Hauser H., Jagels K., Moule S., Norbertczak H.,
RA Ormond D., Price C., Quail M.A., Sanders M., Walker D., Whitehead S.,
RA Salmond G.P.C., Birch P.R.J., Parkhill J., Toth I.K.;
RT "Genome sequence of the enterobacterial phytopathogen Erwinia
carotovora subsp. atroseptica and characterization of virulence
factors.";
RT Proc. Natl. Acad. Sci. U.S.A. 101:11105-11110 (2004).
CC 1- FUNCTION: Could be a mediator in iron transactions between iron
acquisition and iron-requiring processes, such as synthesis and/or
repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC 1- SUBUNIT: Monomer (By similarity).
CC 1- SIMILARITY: Belongs to the Fe(2+)-trafficking protein family.
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CC -----
DR ENBL; BX950851; CAG73886.1; -; Genomic_DNA.
DR SNR; Q6D8J9; 1-87.
DR GenomeReviews; BX950851_GR; ECA0975.
DR HAMAP; MF_00686; -; 1.
DR InterPro; IPR007457; YggX.
DR Pfam; PF04362; Iron traffic; 1.
DR PIRSF; PIRSF029827; Fe traffic_YggX; 1.
DR ProDom; PD029191; DUF495; 1.
DR Complete proteome; Iron.
FT CHAIN 1 90
FT FTID=PRO 0000214481.
SQ SEQUENCE 90 AA; 10640 MW; 9B295D34E542D8A3 CRC64;

Query Match 84.6%; Score 411; DB 1; Length 90;
Best Local Similarity 87.4%; Pred. No. 3.5e-34;
Matches 76; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 1 MSRTICTFLQREAGQDFQYFGELGKRIYNEISKEAWAQWQHKTMLINEKLNMMNA 60
DB 1 MSRTICTVLQREAGQDFQYFGELGKRIYNEISKEAWAQWQHKTMLINEKLNMMNV 60
QY 61 EHRKLEQEMVNFPEGKEVHIEGYTP 87
DB 61 DDKLLEQEMVNFPEGKEVHIEGYTP 87

RESULT 14
FETP YKKPS
ID_FETP YERPS STANDARD; PRT; 90 AA.
AC Q66M3;
DT 19-JUL-2005, integrated into UniProtKB/Swiss-Prot.
DT 11-OCT-2004, sequence version 1.
DT 11-JUL-2006, entry version 13.
DE Probable Fe(2+)-trafficking protein.
GN OrderedLocusNames=YPTB3225;
OS Yersinia pseudotuberculosis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=633;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=IP32953 / Serotype 1;
RX PubMed=15358858; DOI=10.1073/pnas.0404012101;
RA Chai P.S.G., Carniel E., Larivel F.W., Lamerdin J., Stoutland P.O.,
RA Regal W.M., Georgescu A.M., Vergez L.M., Land M.L., Motin V.L.,
RA Brubaker R.R., Fowler J., Hinnebusch J., Marceau M., Medigue C.,
RA Simonet M., Chenal-Francois V., Souza B., Dacheux D., Elliott J.M.,
RA Derbise A., Hauser L.J., Garcia E.;
RT "Insights into the evolution of Yersinia pseudotuberculosis."
Proc. Natl. Acad. Sci. U.S.A. 101:13826-13831(2004).
CC -!- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -!- SUBUNIT: Monomer (By similarity).
CC -!- SIMILARITY: Belongs to the Fe(2+)-trafficking protein family.
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CC -----
DR ENBL; BX936398; CAH22463.1; -; Genomic_DNA.
DR SNR; Q66M3; 1-90.
DR GenomeReviews; BX936398_GR; YPTB3225.
DR HAMAP; MF_00686; -; 1.
DR InterPro; IPR007457; YggX.
DR Pfam; PF04362; Iron traffic; 1.
DR PIRSF; PIRSF029827; Fe traffic_YggX; 1.
DR ProDom; PD029191; DUF495; 1.
DR Complete proteome; Iron.
FT CHAIN 1 90
FT FTID=PRO 0000214520.
SQ SEQUENCE 90 AA; 10608 MW; C7375E7954752B64 CRC64;

Query Match 82.7%; Score 402; DB 1; Length 90;
Best Local Similarity 83.3%; Pred. No. 3e-33;
Matches 75; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 MSRTICTFLQREAGQDFQYFGELGKRIYNEISKEAWAQWQHKTMLINEKLNMMNA 60
DB 1 MARTVETRLQKEADGLDFQYFGELGKRIYNEISKEAWAQWQHKTMLINEKLNMMNDP 60
QY 61 EHRKLEQEMVNFPEGKEVHIEGYTPEDK 90
DB 61 EHRKLEQEMVNFPEGKEVHIEGYTPPAK 90
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Query Match 83.1%; Score 404; DB 1; Length 90;
Best Local Similarity 83.3%; Pred. No. 1.9e-33;
Matches 75; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY 1 MSRTICTFLQREAGQDFQYFGELGKRIYNEISKEAWAQWQHKTMLINEKLNMMNA 60
DB 1 MSRTICTFLQREAGQDFQYFGELGKRIYNEISKEAWAQWQHKTMLINEKLNMMNI 60
QY 61 EHRKLEQEMVNFPEGKEVHIEGYTPEDK 90
DB 61 EDRKLEQEMVNFPEGQDVHIAGYTPPSK 90

RESULT 15
FETP VIBCH
ID_FETP VIBCH STANDARD; PRT; 90 AA.
AC Q9KUR4;
DT 25-JUL-2003, integrated into UniProtKB/Swiss-Prot.
DT 01-OCT-2000, sequence version 1.
DT 25-JUL-2006, entry version 23.
DE Probable Fe(2+)-trafficking protein.
GN OrderedLocusNames=VC0451;
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=666;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 39315 / El Tor Inaba N16961 / Serotype O1;
RX MEDLINE=20406833; PubMed=10952301; DOI=10.1038/35020000;
RA Heidelberg J.F., Eissen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.L.,
RA Ermolaeva M.D., Vamathevan J.J., Bass S., Qin H., Dragoi I.,
RA Sellers P., McDonald L.A., Utterback T.R., Fleischmann R.D.,
RA Nierman W.C., White O., Salzberg S.L., Smith H.O., Colwell R.R.,
RA Mekalanos J.J., Venter J.C., Fraser C.M.;
RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
RT cholerae."
RL Nature 406:477-483(2000).
CC -!- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -!- SIMILARITY: Belongs to the Fe(2+)-trafficking protein family.
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CC -----
DR ENBL; AB004132; AAF93624.1; -; Genomic_DNA.
DR GenomeReviews; AE003852_GR; VC0451.
DR TIGR; VC0451; -.
DR HAMAP; MF_00686; -; 1.
DR InterPro; IPR007457; YggX.
DR Pfam; PF04362; Iron traffic; 1.
DR PIRSF; PIRSF029827; Fe traffic_YggX; 1.
DR ProDom; PD029191; DUF495; 1.
DR Complete proteome; Iron.
FT CHAIN 1 90
FT FTID=PRO 0000214508.
SQ SEQUENCE 90 AA; 10647 MW; 972331B2600B3184 CRC64;

Query Match 82.7%; Score 402; DB 1; Length 90;
Best Local Similarity 83.3%; Pred. No. 3e-33;
Matches 75; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 MSRTICTFLQREAGQDFQYFGELGKRIYNEISKEAWAQWQHKTMLINEKLNMMNA 60
DB 1 MARTVETRLQKEADGLDFQYFGELGKRIYNEISKEAWAQWQHKTMLINEKLNMMNDP 60
QY 61 EHRKLEQEMVNFPEGKEVHIEGYTPEDK 90
DB 61 EHRKLEQEMVNFPEGKEVHIEGYTPPAK 90
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RESULT 16
FETP_VIBVU STANDARD; PRT; 90 AA.
AC Q8DC5;
DT 25-JUL-2003, integrated into UniProtKB/Swiss-Prot.
DT 01-MAR-2003, sequence version 1.
DT 11-JUL-2006, entry version 19.
DE Probable Fe(2+)-trafficking protein.
GN OrderedLocusNames=VW1_1514;
OS Vibrio vulnificus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=672;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=CMCP6;
RA Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,
RA Choy H.B.;
RT Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
RL
CC -!- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -!- SIMILARITY: Belongs to the Fe(2+)-trafficking protein family.
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CC
EMBL; AE016795; AA009940.1; -; Genomic DNA.
DR GenomeReviews; AE016795.GR; VW1_1514.
DR BioCyc; VVUL216895:VV11514-MONOMER; -.
DR HAMAP; MF_00686; -; 1.
DR InterPro; IPR007457; YggX.
DR Pfam; PF04362; Iron_traffic; 1.
DR PRODOM; PD029191; DUF495; 1.
DR Complete proteome; Iron.
KW CHAIN 1 90
FT
FT PROBABILE Fe(2+)-trafficking protein.
FT /FTID=PRO_0000214511.
SQ SEQUENCE 90 AA; 10614 MW; 7EA0CB75840A255C CRC64;
Query Match 82.7%; Score 402; DB 1; Length 90;
Best Local Similarity 82.2%; Pred. No. 3e-33;
Matches 74; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

QY 1 MSRTTCTFLQREAGQDFQLYPGELGKRIYNEISKEAWQHQKOTMLINEKKNMNA 60
DB 1 MSRTTFCARLNKEADGLDFQLYPGELGKRIYNEISKEAWQHQKOTMLINEKKNMNDP 60
QY 61 EHRKLEQEMVNFLEPGKEVHIEGYTPEDK 90
DB 61 EHRKLETEMVNFLEPGKEVHIEGYTPPSK 90

RESULT 17
FETP_VIBVU STANDARD; PRT; 90 AA.
AC Q7MH14;
DT 10-MAY-2004, integrated into UniProtKB/Swiss-Prot.
DT 15-DEC-2003, sequence version 1.
DT 11-JUL-2006, entry version 20.
DE Probable Fe(2+)-trafficking protein.
GN OrderedLocusNames=VW2885;
OS Vibrio vulnificus (strain YJ016).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=196600;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=14656965; DOI=10.1101/gr.1295503;
RA Chen C.-Y., Wu K.-M., Chang Y.-C., Chang A.B.-T., Tsai H.-C.,
RA Liao T.-L., Liu Y.-M., Chen H.-J., Shen A.B.-T., Li J.-C., Su T.-L.,

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RA Shao C.-P., Lee C.-T., Hor L.-I., Tsai S.-P.;
RT "Comparative genome analysis of Vibrio vulnificus, a marine
RL pathogen.";
RL Genome Res. 13:2577-2587(2003).
CC -!- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -!- SIMILARITY: Belongs to the Fe(2+)-trafficking protein family.
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CC
EMBL; BA000037; BAC95649.1; -; Genomic DNA.
DR GenomeReviews; BA000037.GR; VV2885.
DR BioCyc; VVUL196600:VV2885-MONOMER; -.
DR HAMAP; MF_00686; -; 1.
DR InterPro; IPR007457; YggX.
DR Pfam; PF04362; Iron_traffic; 1.
DR PIRSF; PIRSF09827; FeTraffic_YggX; 1.
DR PRODOM; PD029191; DUF495; 1.
DR Complete proteome; Iron.
KW CHAIN 1 90
FT
FT PROBABILE Fe(2+)-trafficking protein.
FT /FTID=PRO_0000214512.
SQ SEQUENCE 90 AA; 10614 MW; 7EA0CB75840A255C CRC64;
Query Match 82.7%; Score 402; DB 1; Length 90;
Best Local Similarity 82.2%; Pred. No. 3e-33;
Matches 74; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

QY 1 MSRTTCTFLQREAGQDFQLYPGELGKRIYNEISKEAWQHQKOTMLINEKKNMNA 60
DB 1 MSRTTFCARLNKEADGLDFQLYPGELGKRIYNEISKEAWQHQKOTMLINEKKNMNDP 60
QY 61 EHRKLEQEMVNFLEPGKEVHIEGYTPEDK 90
DB 61 EHRKLETEMVNFLEPGKEVHIEGYTPPSK 90

RESULT 18
FETP_VIBVU STANDARD; PRT; 90 AA.
AC Q87LI5;
DT 25-JUL-2003, integrated into UniProtKB/Swiss-Prot.
DT 01-JUN-2003, sequence version 1.
DT 11-JUL-2006, entry version 18.
DE Probable Fe(2+)-trafficking protein.
GN OrderedLocusNames=VP2627;
OS Vibrio parahaemolyticus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=670;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=RIMD 2210633 / Serotype O3:K6;
RX MEDLINE=22508454; PubMed=12620739; DOI=10.1016/S0140-6736(03)12659-1;
RA Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
RA Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
RA Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
RT "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
RT distinct from that of V. cholerae.";
RL Lancet 361:743-749(2003).
CC -!- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -!- SIMILARITY: Belongs to the Fe(2+)-trafficking protein family.
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CC
EMBL; BA000031; BAC60890.1; -; Genomic DNA.
DR SMR; Q87LI5; 1-87.
DR GenomeReviews; BA000031.GR; VP2627.
DR HAMAP; MF_00686; -; 1.

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DR InterPro: IPR007457; YggX.
 DR Pfam: PF04362; Iron traffic; 1.
 DR PIRSF: PIRSF029827; Fe traffic_YggX; 1.
 DR ProDom: PD029191; DUF495; 1.
 KW Complete proteome; Iron.
 FT CHAIN 1 90 Probable Fe(2+)-trafficking protein.
 FT /FTid=PRO_0000214510.
 SQ SEQUENCE 90 AA; 10629 MW; A20DS9S35F0F9A1B CRC64;

Query Match 82.1%; Score 399; DB 1; Length 90;
 Best Local Similarity 83.9%; Pred. No. 6e-33;
 Matches 73; Conservative 7; Mismatches 0; Gaps 0;

QY 1 MERTPTCTFLQRAEGDQFLYPGELGKRIYNIISKEAWAQWQHKTMLINEKKNMMA 60
 DB 1 MSRTVFCARLKEGEGDLFLYPGELGKRIYNIISKEAWAQWQHKTMLINEKKNMMDP 60

QY 61 EHRKLEQEMVNFLEFGKDVHIEGYTP 87
 DB 61 EHRKLEQEMVNFLEFGKDVHIEGYTP 87

RESULT 19

Q1V3X2_VIBAL PRELIMINARY; PRT; 90 AA.
 AC Q1V3X2;
 DT 16-MAY-2006, integrated into UniProtKB/TrEMBL.
 DT 16-MAY-2006, sequence version 1.
 DT 11-JUL-2006, entry version 3.
 DE Hypothetical protein.
 GN ORFNames=V12G01_14084;
 OS Vibrio alginolyticus 12G01.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
 OC Vibrionaceae; Vibrrio.
 OX NCBI_TaxID=314288;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=12G01;
 RA Polz M., Ferreira S., Johnson J., Kravitz S., Halpern A.,
 RA Remington K., Beeson K., Tran B., Rogers Y.-H., Friedman R.,
 RA Venter J.C.;
 RL Submitted (MAR-2006) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
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 CC
 CC EMBL; AAPS01000056; EAS74087.1; -; Genomic_DNA.
 DR SMR; Q1V3X2; 1-87.
 DR InterPro: IPR007457; YggX.
 DR Pfam; PF04362; Iron traffic; 1.
 DR PIRSF: PIRSF029827; Fe traffic_YggX; 1.
 DR ProDom; PD029191; DUF495; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 90 AA; 10629 MW; A75D0C535F0F9A1B CRC64;

Query Match 81.7%; Score 397; DB 2; Length 90;
 Best Local Similarity 82.8%; Pred. No. 9.7e-33;
 Matches 72; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY 1 MERTPTCTFLQRAEGDQFLYPGELGKRIYNIISKEAWAQWQHKTMLINEKKNMMA 60
 DB 1 MSRTVFCARLKEGEGDLFLYPGELGKRIYNIISKEAWAQWQHKTMLINEKKNMMDP 60

QY 61 EHRKLEQEMVNFLEFGKDVHIEGYTP 87
 DB 61 EHRKLEQEMVNFLEFGKDVHIEGYTP 87

RESULT 20

FETP_YERPE STANDARD; PRT; 90 AA.
 Q8ZHE7;
 DT 25-JUL-2003, integrated into UniProtKB/Swiss-Prot.
 DT 01-MAR-2002, sequence version 1.
 DT 11-JUL-2006, entry version 30.
 DE Probable Fe(2+)-trafficking protein.
 GN OrderedLocusNames=YPO0953, Y3340, YP3488;
 OS Yersinia pestis.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Yersinia.
 OX NCBI_TaxID=632;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=CO-92 / Biovar Orientalis;
 RX MEDLINE=21470413; PubMed=11586360; DOI=10.1038/35097083;
 RA Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
 RA Prentice M.B., Sebahia M., James K.D., Churcher C.M., Mungall K.L.,
 RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdano-Tarraga A.-M.,
 RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
 RA Feltham T., Hamlin N., Holroyd S., Jagers K., Karlyshev A.V.,
 RA Leather S., Moule S., Oyston P.C.F., Quail M.A., Rutherford K.M.,
 RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
 RT "Genome sequence of Yersinia pestis, the causative agent of plague."
 RL Nature 413:523-527(2001).
 RN [2]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=KIMS / Biovar Mediaevalis;
 RX MEDLINE=22137863; PubMed=12142430;
 RX DOI=10.1128/JB.184.16.4601-4611.2002;
 RA Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,
 RA Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
 RA Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
 RA Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
 RA Perry R.D.;
 RT "Genome sequence of Yersinia pestis KIM."
 RL J. Bacteriol. 184:4601-4611(2002).
 RN [3]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=91001 / Biovar Mediaevalis;
 RX PubMed=15368893; DOI=10.1093/dnares/11.3.179;
 RA Song Y., Tong Z., Wang J., Wang L., Guo Z., Han Y., Zhang J., Pei D.,
 RA Zhou D., Qin H., Pang X., Han Y., Zhai J., Li M., Cui B., Qi Z.,
 RA Jin L., Dai R., Chen F., Li S., Ye C., Du Z., Lin W., Wang J., Yu J.,
 RA Yang H., Wang J., Huang P., Yang R.;
 RT "Complete genome sequence of Yersinia pestis strain 91001, an isolate
 RT avirulent to humans."
 RL DNA Res. 11:179-197(2004).
 CC -!- FUNCTION: Could be a mediator in iron transactions between iron
 CC acquisition and iron-requiring processes, such as synthesis and/or
 CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
 CC -!- SUBUNIT: Monomer (By similarity).
 CC -!- SIMILARITY: Belongs to the Fe(2+)-trafficking protein family.
 CC
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 CC
 CC EMBL; AJ414145; CAC89796.1; -; Genomic_DNA.
 DR EMBL; AE009952; AAM86890.1; -; Genomic_DNA.
 DR EMBL; AE017140; AAS63643.1; -; Genomic_DNA.
 DR SMR; Q8ZHE7; 1-90.
 DR GenomeReviews; AE009952; GR; Y3340.
 DR GenomeReviews; AE017042; GR; YP3488.
 DR GenomeReviews; AL590842; GR; YPO0953.
 DR BioCyc; YPES187410.Y3340-MONOMER; -.
 DR BioCyc; YPES6332.YPO0953-MONOMER; -.
 DR HAMAP; MF_00686; -; 1.
 DR InterPro; IPR007457; YggX.
 DR Pfam; PF04362; Iron traffic; 1.
 DR PIRSF: PIRSF029827; Fe traffic_YggX; 1.
 DR ProDom; PD029191; DUF495; 1.
 KW Complete proteome; Iron.
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Query Match      81.5%; Score 396; DB 1; Length 90;
Best Local Similarity 82.2%; Pred. No. 1.2e-32;
Matches 74; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

QY 1 MSTTICTFLOREAGQDFQLPGELGKRIYNEISKEAWQHQKOTMLINEKKLMMNNA 60
Db 1 MSTTICTFLKDAERQDFQLPGELGKRIYNEISKEAWSQITKOTMLINEKKLSMMNI 60

QY 61 EHRKLEQEMVNFLEPGKGVHIEGYTPEDK 90
Db 61 EDRKLEQEMVNFLEPGQDVHIAGYTPPSK 90

RESULT 21
Q1CEV2_YERPE PRELIMINARY; PRT; 90 AA.
AC Q1CEV2_YERPE
DT 11-JUL-2006, integrated into UniProtKB/TrEMBL.
DT 11-JUL-2006, sequence version 1.
DE Hypothetical protein.
GN ORFNames=YPN_3151;
OS Yersinia pestis Nepal516.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=377628;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Nepal516;
RX PubMed=16740952; DOI=10.1128/JB.00124-06;
RA Chain P.S., Hu P., Malfatti S.A., Radnedge L., Larimer F.,
RA Verges L.M., Worsham P., Chu M.C., Andersen G.L.;
RT "Complete Genome Sequence of Yersinia pestis Strains Antiqua and
RT Nepal516: Evidence of Gene Reduction in an Emerging Pathogen.";
RL J. Bacteriol. 188:4453-4463(2006).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Antiqua;
RG US DOE Joint Genome Institute;
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler J.C.,
RA Glavina del Rio T., Hammon N., Dalin E., Tice H., Pitluck S.,
RA Chain P., Hu P., Malfatti S.A., Radnedge L., Verges L.M., Larimer F.,
RA Land M., Hauser L., Worsham P., Chu M.C., Andersen G.L.,
RA Richardson P.;
RT "Complete sequence of chromosome of Yersinia pestis Antiqua.";
RL Submitted (APR-2006) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; CP000305; ABG19478.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 90 AA; 10707 MW; C7374E6855653F65 CRC64;

Query Match      81.5%; Score 396; DB 2; Length 90;
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QY 1 MSTTICTFLOREAGQDFQLPGELGKRIYNEISKEAWQHQKOTMLINEKKLMMNNA 60
Db 1 MSTTICTFLKDAERQDFQLPGELGKRIYNEISKEAWSQITKOTMLINEKKLSMMNI 60

QY 61 EHRKLEQEMVNFLEPGKGVHIEGYTPEDK 90
Db 61 EDRKLEQEMVNFLEPGQDVHIAGYTPPSK 90

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AC Q1CB93_YERPE
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DT 11-JUL-2006, sequence version 1.
DE Hypothetical protein.
GN ORFNames=YPA_0311;
OS Yersinia pestis Antiqua.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=360102;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Antiqua;
RX PubMed=16740952; DOI=10.1128/JB.00124-06;
RA Chain P.S., Hu P., Malfatti S.A., Radnedge L., Larimer F.,
RA Verges L.M., Worsham P., Chu M.C., Andersen G.L.;
RT "Complete Genome Sequence of Yersinia pestis Strains Antiqua and
RT Nepal516: Evidence of Gene Reduction in an Emerging Pathogen.";
RL J. Bacteriol. 188:4453-4463(2006).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Antiqua;
RG US DOE Joint Genome Institute;
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler J.C.,
RA Glavina del Rio T., Hammon N., Dalin E., Tice H., Pitluck S.,
RA Chain P., Hu P., Malfatti S.A., Radnedge L., Verges L.M., Larimer F.,
RA Land M., Hauser L., Worsham P., Chu M.C., Andersen G.L.,
RA Richardson P.;
RT "Complete sequence of chromosome of Yersinia pestis Antiqua.";
RL Submitted (APR-2006) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; CP000308; ABG12279.1; -; Genomic_DNA.
KW Hypothetical protein.
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QY 1 MSTTICTFLOREAGQDFQLPGELGKRIYNEISKEAWQHQKOTMLINEKKLMMNNA 60
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QY 61 EHRKLEQEMVNFLEPGKGVHIEGYTPEDK 90
Db 61 EDRKLEQEMVNFLEPGQDVHIAGYTPPSK 90

RESULT 23
FETP_SODGM STANDARD; PRT; 90 AA.
AC Q2NRB4;
DT 11-JUL-2006, integrated into UniProtKB/Swiss-Prot.
DT 07-FEB-2006, sequence version 1.
DE Probable Fe(2+)-trafficking protein.
GN OrderedLocNames=SG2036;
OS Sodalis glossinidius (strain morsitans).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Sodalis.
OX NCBI_TaxID=343509;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=16365377; DOI=10.1101/gr.4106106;
RA Toh H., Weiss B.L., Perkin S.A.H., Yamashita A., Oshima K.,
RA Hattori M., Aksoy S.;
RT "Massive genome erosion and functional adaptations provide insights
RT into the symbiotic lifestyle of Sodalis glossinidius in the tsetse
RL host.";
RL Genome Res. 16:149-156(2006).
CC -!- FUNCTION: Could be a mediator in iron transactions between iron
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CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -!- SUBUNIT: Monomer (By similarity).
CC -!- SIMILARITY: Belongs to the Fe(2+)-trafficking protein family.
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CC
CC -----
DR EMBL: AP008232; BAE75311.1; -, Genomic_DNA.
DR SMR: Q2NRB4; 1-87.
DR GenomeReviews; AP008232_GR; SG2036.
DR HAMAP; MF_00686; -, 1.
DR InterPro; IPR007457; YggX.
DR Pfam; PF04362; Iron traffic; 1.
DR PIRSF; PIRSF029827; Fe traffic_YggX; 1.
DR ProDom; PD029191; DUF495; 1.
KW Complete proteome; Iron.
FT CHAIN 1 90
FT Probable Fe(2+)-trafficking protein.
FT /FTId=PRO 0000246119.
SQ SEQUENCE 90 AA; 10701 MW; E9016C38A5D05394 CRC64;

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DB 1 MSTRTICTFLQREAGQDFOLYPGELGKRIYNEISKEAWAQHOKTMLINEKLLNMNA 60
QY 61 EHRKLEQEMVNFLEFGKVEHIEGYTP 87
DB 61 ADRKLEQEMVNFLEFGQDVHIEGYTP 87

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AC Q65VT7;
DT 25-OCT-2005, integrated into UniProtKB/Swiss-Prot.
DT 25-OCT-2004, sequence version 1.
DT 11-JUL-2006, entry version 12.
DE Probable Fe(2+)-trafficking protein.
GN OrderedLocusNames=MS0316;
OS Mannheimia succiniciproducens (strain MB5L55E).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Mannheimia.
OX NCBI_TaxID=221988;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15378067; DOI=10.1038/nbt1010;
RA Hong S.H., Kim J.S., Lee S.Y., In Y.H., Choi S.S., Rih J.-K.,
RA Kim C.H., Jeong H., Hur C.G., Kim J.J.;
RT "The genome sequence of the capnophilic rumen bacterium Mannheimia
RT succiniciproducens".
RL Nat. Biotechnol. 22:1275-1281(2004).
CC -!- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -!- SIMILARITY: Belongs to the Fe(2+)-trafficking protein family.
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CC -----
DR EMBL: AB016827; AAU36923.1; -, Genomic_DNA.
DR SMR: Q65VT7; 1-88.
DR GenomeReviews; AB016827_GR; MS0316.
DR HAMAP; MF_00686; -, 1.
DR InterPro; IPR007457; YggX.
DR Pfam; PF04362; Iron traffic; 1.
DR PIRSF; PIRSF029827; Fe traffic_YggX; 1.
DR ProDom; PD029191; DUF495; 1.
KW Complete proteome; Iron.
FT CHAIN 1 91
FT Probable Fe(2+)-trafficking protein.

FT SEQUENCE 91 AA; 10801 MW; /FTId=PRO 0000214489.
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DB 61 DHRKLEQEMVNFLEFGKDVHIEGYTP 88

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ID FETP HAEI8 STANDARD; PRT; 90 AA.
AC Q4QMD9;
DT 11-JUL-2006, integrated into UniProtKB/Swiss-Prot.
DT 19-JUL-2005, sequence version 1.
DT 11-JUL-2006, entry version 7.
DE Probable Fe(2+)-trafficking protein.
GN OrderedLocusNames=NTHI0920;
OS Haemophilus influenzae (strain 86-028NP).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=281310;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15968074; DOI=10.1128/JB.187.13.4627-4636.2005;
RA Harrison A., Dyer D.W., Gillaspay A., Ray W.C., Mungur R., Carson M.B.,
RA Zhong H., Gipson J., Gipson M., Johnson L.S., Lewis L., Bakaletz L.O.,
RA Munson R.S. Jr.;
RT "Genomic sequence of an otitis media isolate of nontypeable
RT Haemophilus influenzae: comparative study with H. influenzae serotype
RT d, strain KW20".
RL J. Bacteriol. 187:4627-4636(2005).
CC -!- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -!- SIMILARITY: Belongs to the Fe(2+)-trafficking protein family.
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CC -----
DR EMBL: CP000057; AAX87808.1; -, Genomic_DNA.
DR SMR: Q4QMD9; 1-87.
DR GenomeReviews; CP000057_GR; NTHI0920.
DR HAMAP; MF_00686; -, 1.
DR InterPro; IPR007457; YggX.
DR Pfam; PF04362; Iron traffic; 1.
DR PIRSF; PIRSF029827; Fe traffic_YggX; 1.
DR ProDom; PD029191; DUF495; 1.
KW Complete proteome; Iron.
FT CHAIN 1 90
FT Probable Fe(2+)-trafficking protein.
FT /FTId=PRO 0000246101.
SQ SEQUENCE 90 AA; 10582 MW; EB34CEFF737B93B CRC64;

Query Match 79.6%; Score 387; DB 1; Length 90;
Best Local Similarity 78.2%; Pred. No. 1e-31;
Matches 68; Conservative 12; Mismatches 7; Indels 0; Gaps 0;

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DB 1 MARTVFCRYLKREAGELDFOLYPGELGKRIYNEISKEAWAQHOKTMLINEKLLNMNA 60
QY 61 EHRKLEQEMVNFLEFGKVEHIEGYTP 87
DB 61 EHRKLEQEMVNFLEFGKDVHIEGYTP 87

Search completed: June 27, 2007, 11:10:39
Job time : 349 secs

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OM protein - protein search, using sw model

Run on: June 27, 2007, 11:10:57 ; Search time 50 Seconds
(without alignments)
159.306 Million cell updates/sec

Title: US-09-955-502A-11

Perfect score: 486

Sequence: 1 MSRIFFCTFLQREAGQDFQ.....NFLPFGKVHIEGYTPDKK 91

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

Database : Issued Patents_AA.*

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2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep.*

3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep.*

4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep.*

5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PTUS_COMB.pep.*

6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep.*

7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	450	92.6	107	2	US-09-489-039A-11962
2	389	80.0	93	2	US-09-543-681A-5443
3	231	47.5	122	2	US-09-252-991A-23355
4	199.5	41.0	92	2	US-09-328-352-5456
5	131	27.0	110	2	US-09-540-236-2859
6	76	15.6	548	2	US-09-167-299-3
7	72	14.8	474	2	US-09-252-991A-24473
8	70.5	14.5	1214	2	US-10-164-595-24
9	67.5	13.9	184	2	US-09-325-932A-66
10	67.5	13.9	546	1	US-08-533-669A-2
11	67.5	13.9	546	2	US-09-183-861-2
12	67.5	13.9	546	2	US-09-022-765-2
13	67.5	13.9	546	2	US-09-551-974A-2
14	67.5	13.9	546	2	US-09-565-501A-2
15	67.5	13.9	546	2	US-09-639-206A-2
16	67.5	13.9	546	2	US-09-874-923-2
17	67.5	13.9	546	2	US-08-798-841-2
18	67.5	13.9	982	2	US-09-551-974A-95
19	67.5	13.9	982	2	US-09-565-501A-95
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22	67.5	13.9	1427	2	US-09-551-974A-97
23	67.5	13.9	1427	2	US-09-565-501A-97
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ALIGNMENTS

RESULT 1

US-09-489-039A-11962
; Sequence 11962, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Berton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709 2004001
; CURRENT APPLICATION NUMBER: US/09/489, 039A
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 11962
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11962

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28	67.5	13.9	1641	2	US-09-639-206A-96	Sequence 96, Appl
29	67.5	13.9	1641	2	US-09-874-923-96	Sequence 96, Appl
30	65.5	13.5	295	2	US-09-914-098-46	Sequence 46, Appl
31	65	13.4	292	2	US-09-328-352-5836	Sequence 5836, Ap
32	64.5	13.3	209	2	US-09-252-991A-20905	Sequence 20905, A
33	64	13.2	227	2	US-09-270-767-58283	Sequence 58283, A
34	64	13.2	280	2	US-09-323-998B-37	Sequence 37, Appl
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37	63.5	13.1	591	2	US-09-370-368-8	Sequence 8, Appl
38	63	13.0	525	2	US-09-540-236-2250	Sequence 2250, Ap
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40	62.5	12.9	325	2	US-09-134-000C-4346	Sequence 4346, Ap
41	62.5	12.9	544	2	US-09-248-796A-18911	Sequence 18911, A
42	62.5	12.9	798	2	US-09-861-451A-12	Sequence 12, Appl
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44	62	12.8	1394	2	US-09-248-796A-19555	Sequence 19555, A
45	62	12.8	1501	2	US-09-710-279-2850	Sequence 2850, Ap
46	62	12.8	1529	2	US-09-134-001C-3945	Sequence 3945, Ap
47	61.5	12.7	57	2	US-09-562-737-124	Sequence 124, App
48	61.5	12.7	116	2	US-09-562-737-125	Sequence 125, App
49	61.5	12.7	311	2	US-09-248-796A-26397	Sequence 26397, A
50	61.5	12.7	419	2	US-09-543-681A-7295	Sequence 7295, Ap
51	61.5	12.7	680	2	US-09-298-924-4	Sequence 4, Appl
52	61.5	12.7	720	1	US-08-840-236-1	Sequence 1, Appl
53	61.5	12.7	720	1	US-08-505-448A-1	Sequence 1004, Ap
54	61	12.6	308	2	US-09-198-452A-1004	Sequence 16, Appl
55	61	12.6	444	2	US-09-861-451A-16	Sequence 934, App
56	61	12.6	480	2	US-09-438-185A-934	Sequence 4802, Ap
57	60.5	12.4	139	2	US-09-513-999C-4802	Sequence 4800, Ap
58	60.5	12.4	258	2	US-09-513-999C-4800	Sequence 6012, Ap
59	60.5	12.4	264	2	US-09-949-016-6012	Sequence 11703, A
60	60.5	12.4	276	2	US-09-949-016-11703	Sequence 48, Appl
61	60.5	12.4	404	2	US-09-914-098-48	Sequence 2, Appl
62	60.5	12.4	640	2	US-09-873-404-2	Sequence 2, Appl
63	60.5	12.4	640	2	US-10-243-735-2	Sequence 7, Appl
64	60.5	12.4	640	2	US-10-730-010-2	Sequence 41085, A
65	60.5	12.4	1076	2	US-09-171-991-7	Sequence 56301, A
66	60	12.3	98	2	US-09-270-767-61085	Sequence 19265, A
67	60	12.3	98	2	US-09-270-767-56301	Sequence 221, App
68	60	12.3	184	2	US-09-248-796A-19265	Sequence 205, App
69	60	12.3	271	2	US-09-198-452A-221	Sequence 6400, Ap
70	60	12.3	279	2	US-09-438-185A-205	Sequence 41746, A
71	60	12.3	331	2	US-09-328-352-6400	Sequence 46116, A
72	60	12.3	337	2	US-09-270-767-41746	Sequence 8705, Ap
73	60	12.3	337	2	US-09-270-767-46116	
74	60	12.3	389	2	US-09-270-767-46116	
75	60	12.3	410	2	US-09-949-016-8705	

Query Match 92.6%; Score 450; DB 2; Length 107;
Best Local Similarity 91.2%; Pred. No. 1.e-48;
Matches 83; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY

MSRTIFCTFLQRAEGQDFQLYPGELGKRIYEISKEAWAQWHKQTMLINEKLNMNA 60
||||| : ||||| : ||||| :

Dd

MSRTIFCTFLQREADGDFFQLYPGELGKRIYEISKEAWAQWHKQTMLINEKLNNMP 76

Qy 61 EHRKLEQEMVNFLFEGKEVHIEGYTPEDKK 91
 |||||
 Dp 77 EHRKLEQEMVOLFEGKDVHIEGYTPPEKO 107
 |||||

```

RESULT 2
US-09-543-681A-5443
; Sequence 5443, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 5443
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-5443

```

```
Query Match      80.0%; Score 389; DB 2; Length 93;
Best Local Similarity 80.0%; Pred. No. 4.2e-41;
Matches 72; Conservative 7; Mismatches 11; Indels 0; Gaps 0;
```

Qy

1	MSRTIFCTFLQRAEGDPQLYPGELGRIFYNEISKEAWAQWQHQTMLINEKLNMA	60
: : : : : : : :		

Dd

4	MSRTIFCTFLNKGADGLDLPOLYPGELGRIFYNEISKEAWGWAKOTMLINEKLNTWP	63
: : : : : : : :		

QY 61 EHRKLLQEVMVNFLEGGKEVHIEGYTPEDK 90
: ||||| ||||| : ||| : |
Db 64 DDRKLLQEVMVNFLEGGHVDHIDGYTPPEK 93

```

RESULT 3
US-09-252-991A-23355
; Sequence 23355, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23355
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23355

```

Query Match 47.5%; Score 231; DB 2; Length 122;
Best Local Similarity 51.7%; Pred. No. 3.9e-21;
Matches 45; Conservative 10; Mismatches 32; Indels 0; Gaps 0;

1 MSTITCTFLQREAGDFQLYPGLGRLIYNEISKEAWAOWHKQOTMLINEKLIANNNA 60
33 MSRTVMCRKTHEELPGLDRPPYPAKGSIDIYNNVRKAWDEWQHQOTMLINERRLIANNNA 92
61 EHRKLLLEQEMVNFLEFGKEVHIEGYTP 87
93 EDRKFLQCEMDKFLSGEDYAKADGYTP 119

RESULT 4
 US-09-328-352-5456
 ; Sequence 5456, Application US/09328352
 ; Patent No. 6562958
 ; GENERAL INFORMATION:
 ; APPLICANT: Gary L. Breton et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
 ; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: GTC99-03PA
 ; CURRENT APPLICATION NUMBER: US/09/328,352
 ; CURRENT FILING DATE: 1999-06-04
 ; NUMBER OF SEQ ID NOS: 8252
 ; SEQ ID NO 5456
 ; LENGTH: 92
 ; TYPE: PRT
 ; ORGANISM: Acinetobacter baumannii
 US-09-328-352-5456

Query Match 41.0%; Score 199.5; DB 2; Length 92;
Best Local Similarity 42.7%; Pred. No. 2.4e-17;
Matches 38; Conservative 15; Mismatches 35; Indels 1; Caps 1;

[illegible]

Qy 61 EHRKLLQEAMVNFLEFEGEVH-IEGYTPE 88
| : | | : | : |
Dp 64 EAKKFLFEOREKFENDESVEKAEGWKPE 92
| : | | : | : |

```

RESULT 5
US-09-540-236-2859
; Sequence 2859, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQU
; FILE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 2859
; LENGTH: 110
; TYPE: PRT
; ORGANISM: M.catarrhalis
US-09-540-236-2859

```

```

Query Match      27.0%; Score 131; DB 2; Length 110;
Best Local Similarity 34.9%; Pred. No. 1.2e-08;
Matches 29; Conservative 13; Mismatches 41; Indels 0; Gaps 0

5  IFTFLQREAGQDFQLYPGBLGKRIYNEISKEAWAQHQTMLINEKUNMNAEHRK 64
   ||| : : : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
25 VFCKRYQQNLPLKLPNPPFNAGQGEIQDTISAKAWNAWLEQTMLINEKHLSPIDPQAK 84
   ||| : : : ||| : ||| : ||| : ||| : ||| : ||| : ||| :

65 LLEQEMVNFLEPGKEVHIEGYTP 87
   ||| : : : ||| : ||| : ||| : ||| : ||| : ||| : ||| :

85 YLNEOREKFLDNGDYKPYAGYKP 107
   ||| : : : ||| : ||| : ||| : ||| : ||| : ||| : ||| :

```

RESULT 6
US-09-167-299-3

```

: Sequence 3. Application US/09167299
: Patent No. 6245533
: GENERAL INFORMATION:
: APPLICANT: Kron, Micheal
: APPLICANT: Hartlein, Micheal
: APPLICANT: Michitko, Hikakata
: TITLE OF INVENTION: Human Asparaginase
: FILE REFERENCE: Apatraginyl-trna SVY
: CURRENT APPLICATION NUMBER: US/09/
: CURRENT FILING DATE: 1998-10-06
: NUMBER OF SEQ ID NOS: 7
: SOFTWARE: Patentin Ver. 2.0
: SEQ ID NO 3
: LENGTH: 548
: TYPE: PRT
: ORGANISM: Brugia malayi
: PUBLICATION INFORMATION:
: DATABASE ACCESSION NUMBER: p10723
: DATABASE ENTRY DATE: 1997-11-01
: US-09-167-299-3

```

[illegible]

```

RESULT 7
US-09-252-991A-24473
; Sequence 24473, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 24473
; LENGTH: 474
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-24473

```

```

Query Match      14.8%; Score 72; DB 2; Length 474;
Best Local Similarity 25.6%; Pred. No. 2;
Matches 20; Conservative 18; Mismatches 28; Indels 12; Gaps 3;

QY 13 EAQGDFQLYP-----GELGRI-YNEISKEAWAQHQKOTMLINEKLMNMNAEHRKL 65
      ||| ||| ||| : : : : : ||| : : : : : ||| : : : : :
Db 299 ELEAPSLDAYPEIWEAGSARAVLDKTIPEVQSKPGKTELLNGKLTGRDAAHKR- 357.

QY 66 LEQEMNFLPEGKGVHIE 83
      ||| : : : : :
Db 358 ----MVDMLNKGETLLPVD 371

```

RESULT 8
US-10-164-595-24
; Sequence 24, Application US/10164595
; Patent No. 6657054

```

; GENERAL INFORMATION:
; APPLICANT: Origene Technologies, Inc
; TITLE OF INVENTION: Regulated Angiogenesis Genes and Polypeptides
; FILE REFERENCE: 1U 103 R1
; CURRENT APPLICATION NUMBER: US/10/164,595
; CURRENT FILING DATE: 2002-06-10
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 1214
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-164-595-24

```

```

Query Match      14.5%  Score 70.5;  DB 2;  Length 1214;
Best Local Similarity 28.4%;  Pred. No. 11;
Matches 23;  Conservative 10;  Mismatches 29;  Indels 19;  Gaps 2;

Qy      30  IYNEISKEAWA-----QWQHQTMLINEKLNMMNAHEHKLLEQWVNF 73
      |||:|||||
Db      944  IYNDLSKNTGGTIAETRRRLRIETKQLQWLHQEELSEMKNLELTMAEMRQSLQEQRDL 1003
      |||:|||||

Qy      74  LFEGK----EVHIEGYTPEDKK 91
      |||:|:|:|
Db      1004  IAEVTKQLELEKQQAVDETKK 1024
      |||:|:|:|

```

```

RESULT 9
US-09-325-932A-66
; Sequence 66, Application US/09325932A
; Patent No. 6451604
; GENERAL INFORMATION:
; APPLICANT: Flinn, Barry
; APPLICANT: Lasham, Annette
; TITLE OF INVENTION: Compositions aff
; FILE OF INVENTION: death and their
; FILE REFERENCE: 1032
; CURRENT APPLICATION NUMBER: US/09/325
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 206
; SOFTWARE: FastSeq for Windows Versio
; SEQ ID NO 66
; LENGTH: 184
; TYPE: PrT
; ORGANISM: Pinus radiata
US-09-325-932A-66

```

	Query Match	13.9%; Score 67.5; DB 2;	Length 184;
	Best Local Similarity	25.2%; Pred.No. 2.1;	
	Matches	34; Conservative 14; Mismatches 34;	Indels 53; Gaps 6;
Qy	8 TFLOREAGGD-FQLYPGELGKLYNEISKE-----AWAQOH	44	
Dd	42 TAAQRKVROSFPQFYEDLLKLLESELSDFFKA VFLWVLDPAERDAVTSHGAIKKWNA	101	
Qy	45 KQTMLIN-----EKKLNMMAEH-----RKLLQEOMVNFLPEGG	78	
Dd	102 KNLSLEISSARSAELLMVRYQHRYTKSLREDVAHTSGNFRKLLVALVSSYRVEGP	161	
Qy	79 EV--HIEGYTPDEKK	91	
Dd	162 EVDVMHLASY--EAKK	174	

RESULT 10
US-08-533-669A-2
; Sequence 2, Application US/08533669A
; Patent No. 5834592
; GENERAL INFORMATION:
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
; THERAPY AND DIAGNOSIS OF LEISHMANIASIS
; NUMBER OF SEQUENCES: 18

```
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/533,669A
; FILING DATE: 22-SEP-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.420
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 546 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-533-669A-2

Query Match 13.9%; Score 67.5; DB 1; Length 546;
Best Local Similarity 28.3%; Pred. No. 8.9;
Matches 26; Conservative 12; Mismatches 33; Indels 21; Gaps 5;

QY 1 MSRTIFCTFLQREAGQDFQLPGELGKRIYNEISKEAWAQHQTMLINEKKNMNA 60
Db 301 MTRNALCLQRQRYEAA-IDLY-----KRALVWRNPDTL----KLTCECK 342
QY 61 EHRKLEQMVNLFEGKEVHIEG--YTPEDK 90
Db 343 EHQAEEAYIDPEI-AKQKDEGNQYFKEDK 373

RESULT 11
US-09-183-861-2
; Sequence 2, Application US/09183861
; Patent No. 6385165
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Webb, John R.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Skeiky, Yasir A.W.
; TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USEIN THE THERAPY AND
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/183,861
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
```

```
; APPLICATION NUMBER: 09/022,765
; FILING DATE: 12-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.420C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 546 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-183-861-2

Query Match 13.9%; Score 67.5; DB 2; Length 546;
Best Local Similarity 28.3%; Pred. No. 8.9;
Matches 26; Conservative 12; Mismatches 33; Indels 21; Gaps 5;

QY 1 MSRTIFCTFLQREAGQDFQLPGELGKRIYNEISKEAWAQHQTMLINEKKNMNA 60
Db 301 MTRNALCLQRQRYEAA-IDLY-----KRALVWRNPDTL----KLTCECK 342
QY 61 EHRKLEQMVNLFEGKEVHIEG--YTPEDK 90
Db 343 EHQAEEAYIDPEI-AKQKDEGNQYFKEDK 373

RESULT 12
US-09-022-765-2
; Sequence 2, Application US/09022765
; Patent No. 6375955
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Webb, John R.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Skeiky, Yasir A.W.
; TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USEIN THE THERAPY AND
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,765
; FILING DATE: 12-FEB-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.420C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 546 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-022-765-2
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```

US-09-565-501A-2
Query Match      13.9%; Score 67.5; DB 2; Length 546;
Best Local Similarity 28.3%; Pred.No.8.9;
Matches 26; Conservative 12; Mismatches 33; Indels 21; Gaps 5;

QY      1 MSRTICTFLORAEAGDGFOLYPCELGKRIYNISKEAWAQOHKOTMLINEKKLNMMNA 60
DB      301 MTNRNALCLOQRKYEA--IDLY-----KRALVEWRNPDTL----KKLTECEK 342

QY      61 EHRKLLEQEMVNFPEGKEVHIEG--YTPEDK 90
DB      343 EHQAIVEAYIDPEI-AKQKDSEGNQYFKEDK 373

RESULT 15
US-09-639-206A-2
; Sequence 2, Application US/09639206A
; Patent No. 661337
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Webb, John R.
; APPLICANT: Dillion, Davin C.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Bhatia, Ajay
; APPLICANT: Coler, Rhea
; APPLICANT: Probst, Peter
; TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF LEISHMANIASIS
; FILE REFERENCE: 210121.420C7
; CURRENT APPLICATION NUMBER: US/09/639,206A
; CURRENT FILING DATE: 2000-08-14
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 546
; TYPE: PRT
; ORGANISM: Leishmania major
US-09-639-206A-2

Query Match      13.9%; Score 67.5; DB 2; Length 546;
Best Local Similarity 28.3%; Pred.No.8.9;
Matches 26; Conservative 12; Mismatches 33; Indels 21; Gaps 5;

QY      1 MSRTICTFLORAEAGDGFOLYPCELGKRIYNISKEAWAQOHKOTMLINEKKLNMMNA 60
DB      301 MTNRNALCLOQRKYEA--IDLY-----KRALVEWRNPDTL----KKLTECEK 342

QY      61 EHRKLLEQEMVNFPEGKEVHIEG--YTPEDK 90
DB      343 EHQAIVEAYIDPEI-AKQKDSEGNQYFKEDK 373

RESULT 16
US-09-874-923-2
; Sequence 2, Application US/09874923
; Patent No. 6638517
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Webb, John R.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Bhatia, Ajay
; APPLICANT: Coler, Rhea
; APPLICANT: Probst, Peter
; APPLICANT: Brannon, Mark
; TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF LEISHMANIASIS
; FILE REFERENCE: 210121.420C8
; CURRENT APPLICATION NUMBER: US/09/874,923
; CURRENT FILING DATE: 2001-06-04

```

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; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 546
; TYPE: PRT
; ORGANISM: Leishmania major
US-09-874-923-2

Query Match      13.9%; Score 67.5; DB 2; Length 546;
Best Local Similarity 28.3%; Pred. No. 8.9;
Matches 26; Conservative 12; Mismatches 33; Indels 21; Gaps 5;

QY 1 MSTTFTFLQREAGQDFOLYPGELGKRIYNEISKEAWAQWQHKTMLINEKLNMMNA 60
Db 301 MTRNALCLQRKYEA--IDLY-----KRALVWRNPDTL-----KKLTECEK 342

QY 61 EHRKLEQEMVNFLEFGKEVHIEG--YTPEDK 90
Db 343 EHQKAVEAYIDPEI-AKQKDEGNQYFKEDK 373

RESULT 17
US-08-798-841-2
; Sequence 2, Application US/08798841
; Patent No. 6709661
; GENERAL INFORMATION:
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
; THERAPY AND DIAGNOSIS OF LEISHMANIASIS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/798,841
; FILING DATE: 12-FEB-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.420C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 546 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-798-841-2

Query Match      13.9%; Score 67.5; DB 2; Length 546;
Best Local Similarity 28.3%; Pred. No. 8.9;
Matches 26; Conservative 12; Mismatches 33; Indels 21; Gaps 5;

QY 1 MSTTFTFLQREAGQDFOLYPGELGKRIYNEISKEAWAQWQHKTMLINEKLNMMNA 60
Db 301 MTRNALCLQRKYEA--IDLY-----KRALVWRNPDTL-----KKLTECEK 342

QY 61 EHRKLEQEMVNFLEFGKEVHIEG--YTPEDK 90
Db 343 EHQKAVEAYIDPEI-AKQKDEGNQYFKEDK 373

; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 546
; TYPE: PRT
; ORGANISM: Leishmania major
US-09-874-923-2

Query Match      13.9%; Score 67.5; DB 2; Length 546;
Best Local Similarity 28.3%; Pred. No. 8.9;
Matches 26; Conservative 12; Mismatches 33; Indels 21; Gaps 5;

QY 1 MSTTFTFLQREAGQDFOLYPGELGKRIYNEISKEAWAQWQHKTMLINEKLNMMNA 60
Db 301 MTRNALCLQRKYEA--IDLY-----KRALVWRNPDTL-----KKLTECEK 342

QY 61 EHRKLEQEMVNFLEFGKEVHIEG--YTPEDK 90
Db 343 EHQKAVEAYIDPEI-AKQKDEGNQYFKEDK 373

RESULT 18
US-09-551-974A-95
; Sequence 95, Application US/09551974A
; Patent No. 6500437
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Webb, John R.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Skeiky, Yasir A.W.
; TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
; THERAPY AND DIAGNOSIS OF LEISHMANIASIS
; FILE REFERENCE: 210121.420C5
; CURRENT APPLICATION NUMBER: US/09/551,974A
; CURRENT FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 95
; LENGTH: 982
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion (poly-protein) constructs comprising multiple
; OTHER INFORMATION: Leishmania antigens
US-09-551-974A-95

Query Match      13.9%; Score 67.5; DB 2; Length 982;
Best Local Similarity 28.3%; Pred. No. 19;
Matches 26; Conservative 12; Mismatches 33; Indels 21; Gaps 5;

QY 1 MSTTFTFLQREAGQDFOLYPGELGKRIYNEISKEAWAQWQHKTMLINEKLNMMNA 60
Db 509 MTRNALCLQRKYEA--IDLY-----KRALVWRNPDTL-----KKLTECEK 550

QY 61 EHRKLEQEMVNFLEFGKEVHIEG--YTPEDK 90
Db 551 EHQKAVEAYIDPEI-AKQKDEGNQYFKEDK 581

RESULT 19
US-09-565-501A-95
; Sequence 95, Application US/09565501A
; Patent No. 6607731
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Webb, John R.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Bhatia, Ajay
; APPLICANT: Coler, Rhea
; APPLICANT: Peter Probst
; TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
; THERAPY AND DIAGNOSIS OF LEISHMANIASIS
; FILE REFERENCE: 210121.420C6
; CURRENT APPLICATION NUMBER: US/09/565,501A
; CURRENT FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 95
; LENGTH: 982
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion (poly-protein) constructs comprising multiple
; OTHER INFORMATION: Leishmania antigens
US-09-565-501A-95

Query Match      13.9%; Score 67.5; DB 2; Length 982;
Best Local Similarity 28.3%; Pred. No. 19;
Matches 26; Conservative 12; Mismatches 33; Indels 21; Gaps 5;
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QY 1 MSRTIFCTFLOREAGQDFQLYPGELGKRIYNEISKEAWAQHOKTMTLINEKKNMNA 60
Db 509 MTRNALCLQRQKYEAA-IDLY-----KRALVEWRNPDTL-----KKLTECEK 550
QY 61 EHRKLEQEMVNFPEGKEVHIEG--YTPEDK 90
Db 551 EHQKAVEAYIDPEI-AKQKDEGNQYFKEDK 581

RESULT 20
US-09-639-206A-95
; Sequence 95, Application US/09639206A
; Patent No. 6613337
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Webb, John R.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Bhatia, Ajay
; APPLICANT: Coler, Rhea
; APPLICANT: Probst, Peter
; TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
; FILE REFERENCE: 210121.420C7
; CURRENT APPLICATION NUMBER: US/09/639,206A
; CURRENT FILING DATE: 2000-08-14
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 95
; LENGTH: 982
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion (poly-protein) constructs comprising multiple
; OTHER INFORMATION: Leishmania antigens
US-09-639-206A-95

Query Match 13.9%; Score 67.5; DB 2; Length 982;
Best Local Similarity 28.3%; Pred. No. 19;
Matches 26; Conservative 12; Mismatches 33; Indels 21; Gaps 5;
QY 1 MSRTIFCTFLOREAGQDFQLYPGELGKRIYNEISKEAWAQHOKTMTLINEKKNMNA 60
Db 509 MTRNALCLQRQKYEAA-IDLY-----KRALVEWRNPDTL-----KKLTECEK 550
QY 61 EHRKLEQEMVNFPEGKEVHIEG--YTPEDK 90
Db 551 EHQKAVEAYIDPEI-AKQKDEGNQYFKEDK 581

RESULT 21
US-09-874-923-95
; Sequence 95, Application US/09874923
; Patent No. 6638517
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Webb, John R.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Bhatia, Ajay
; APPLICANT: Coler, Rhea
; APPLICANT: Probst, Peter
; APPLICANT: Brannon, Mark
; TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
; FILE REFERENCE: 210121.420C8
; CURRENT APPLICATION NUMBER: US/09/874,923
; CURRENT FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 95

; LENGTH: 982
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion (poly-protein) constructs comprising multiple
; OTHER INFORMATION: Leishmania antigens
US-09-874-923-95

Query Match 13.9%; Score 67.5; DB 2; Length 982;
Best Local Similarity 28.3%; Pred. No. 19;
Matches 26; Conservative 12; Mismatches 33; Indels 21; Gaps 5;
QY 1 MSRTIFCTFLOREAGQDFQLYPGELGKRIYNEISKEAWAQHOKTMTLINEKKNMNA 60
Db 509 MTRNALCLQRQKYEAA-IDLY-----KRALVEWRNPDTL-----KKLTECEK 550
QY 61 EHRKLEQEMVNFPEGKEVHIEG--YTPEDK 90
Db 551 EHQKAVEAYIDPEI-AKQKDEGNQYFKEDK 581

RESULT 22
US-09-551-974A-97
; Sequence 97, Application US/09551974A
; Patent No. 6500437
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Webb, John R.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Skeiky, Yasir A.W.
; TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
; FILE REFERENCE: 210121.420C5
; CURRENT APPLICATION NUMBER: US/09/551,974A
; CURRENT FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 97
; LENGTH: 1427
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion (poly-protein) constructs comprising multiple
; OTHER INFORMATION: Leishmania antigens
US-09-551-974A-97

Query Match 13.9%; Score 67.5; DB 2; Length 1427;
Best Local Similarity 28.3%; Pred. No. 32;
Matches 26; Conservative 12; Mismatches 33; Indels 21; Gaps 5;
QY 1 MSRTIFCTFLOREAGQDFQLYPGELGKRIYNEISKEAWAQHOKTMTLINEKKNMNA 60
Db 509 MTRNALCLQRQKYEAA-IDLY-----KRALVEWRNPDTL-----KKLTECEK 550
QY 61 EHRKLEQEMVNFPEGKEVHIEG--YTPEDK 90
Db 551 EHQKAVEAYIDPEI-AKQKDEGNQYFKEDK 581

RESULT 23
US-09-565-501A-97
; Sequence 97, Application US/09565501A
; Patent No. 6607731
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Webb, John R.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Bhatia, Ajay
; APPLICANT: Coler, Rhea
; APPLICANT: Peter Probst

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; TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
; FILE REFERENCE: 210121.420C6
; CURRENT APPLICATION NUMBER: US/09/565,501A
; CURRENT FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 97
; LENGTH: 1427
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion (poly-protein) constructs comprising multiple
; OTHER INFORMATION: Leishmania antigens
US-09-565-501A-97

Query Match      13.9%; Score 67.5; DB 2; Length 1427;
Best Local Similarity 28.3%; Pred. No. 32;
Matches 26; Conservative 12; Mismatches 33; Indels 21; Gaps 5;

QY 1 MSTTFTFLQREAGQDFOLYPGELGKRIYNEISKEAWAQHQTMLINEKKLANMNA 60
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 509 MTRNALCLQRQKYEA--IDLY-----KRALVWRNPDTL-----KKLTECEK 550

QY 61 EHRKLEQEMVNFLEFGKEVHIEG--YTPEDK 90
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Db 551 EHQKAVEEAYIDPEI-AKQKDEGNQYFKEDK 581
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RESULT 24
US-09-639-206A-97
; Sequence 97, Application US/09639206A
; Patent No. 6613337
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Webb, John R.
; APPLICANT: Dillion, Davin C.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Bhatia, Ajay
; APPLICANT: Coler, Rhea
; APPLICANT: Probst, Peter
; TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
; FILE REFERENCE: 210121.420C7
; CURRENT APPLICATION NUMBER: US/09/639,206A
; CURRENT FILING DATE: 2000-08-14
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 97
; LENGTH: 1427
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion (poly-protein) constructs comprising multiple
; OTHER INFORMATION: Leishmania antigens
US-09-639-206A-97
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Query Match      13.9%; Score 67.5; DB 2; Length 1427;
Best Local Similarity 28.3%; Pred. No. 32;
Matches 26; Conservative 12; Mismatches 33; Indels 21; Gaps 5;

QY 1 MSTTFTFLQREAGQDFOLYPGELGKRIYNEISKEAWAQHQTMLINEKKLANMNA 60
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 509 MTRNALCLQRQKYEA--IDLY-----KRALVWRNPDTL-----KKLTECEK 550

QY 61 EHRKLEQEMVNFLEFGKEVHIEG--YTPEDK 90
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 551 EHQKAVEEAYIDPEI-AKQKDEGNQYFKEDK 581
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RESULT 25
US-09-874-923-97
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; Sequence 97, Application US/09874923
; Patent No. 6638517
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Webb, John R.
; APPLICANT: Dillion, Davin C.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Bhatia, Ajay
; APPLICANT: Coler, Rhea
; APPLICANT: Probst, Peter
; APPLICANT: Brannon, Mark
; TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
; FILE REFERENCE: 210121.420C8
; CURRENT APPLICATION NUMBER: US/09/874,923
; CURRENT FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 97
; LENGTH: 1427
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion (poly-protein) constructs comprising multiple
; OTHER INFORMATION: Leishmania antigens
US-09-874-923-97

Query Match      13.9%; Score 67.5; DB 2; Length 1427;
Best Local Similarity 28.3%; Pred. No. 32;
Matches 26; Conservative 12; Mismatches 33; Indels 21; Gaps 5;

QY 1 MSTTFTFLQREAGQDFOLYPGELGKRIYNEISKEAWAQHQTMLINEKKLANMNA 60
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 509 MTRNALCLQRQKYEA--IDLY-----KRALVWRNPDTL-----KKLTECEK 550

QY 61 EHRKLEQEMVNFLEFGKEVHIEG--YTPEDK 90
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 551 EHQKAVEEAYIDPEI-AKQKDEGNQYFKEDK 581

Search completed: June 27, 2007, 11:12:21
Job time : 52 secs
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GenCore version 6.2.1
Copyright (c) 1993 - 2007 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: June 27, 2007, 11:23:07 ; Search time 187 Seconds
(without alignments)
225.415 Million cell updates/sec

Title: US-09-955-502A-11
Perfect score: 486
Sequence: 1 MSRTTCTFLQREAGQDFQ.....NFLPFGKEVHIEGYTPDKK 91

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : Published Applications AA_Main:*
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2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
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6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	486	100.0	91	3	US-09-955-502-11
2	486	100.0	91	3	US-09-955-502-12
3	486	100.0	91	3	US-09-955-502-13
4	469	96.5	91	3	US-09-955-502-14
5	469	96.5	91	3	US-09-955-502-15
6	469	96.5	91	3	US-09-955-502-16
7	455	93.6	91	3	US-09-955-502-17
8	453	93.2	88	3	US-09-955-502-18
9	402	82.7	90	3	US-09-955-502-19
10	396	81.5	90	3	US-09-955-502-20
11	395	81.3	78	3	US-09-955-502-21
12	388	79.8	91	3	US-09-955-502-22
13	387	79.6	87	3	US-09-955-502-23
14	379	78.0	87	3	US-09-955-502-24
15	373	76.7	87	3	US-09-955-502-25
16	332	68.3	88	3	US-09-955-502-26
17	265	54.5	76	3	US-09-955-502-27
18	255	52.5	87	3	US-09-955-502-28
19	255	52.5	87	3	US-09-955-502-29
20	241	49.6	86	3	US-09-955-502-30
21	231	47.5	87	3	US-09-955-502-31
22	227	46.7	88	3	US-09-955-502-32
23	227	46.7	90	3	US-09-955-502-33
24	226	46.5	89	3	US-09-955-502-34
25	225	46.3	87	3	US-09-955-502-35
26	213	43.8	88	3	US-09-955-502-36
27	213	43.8	88	3	US-09-955-502-37

28	213	43.8	88	3	US-09-955-502-38	Sequence 28, Appl
29	213	43.8	88	3	US-10-467-657-968	Sequence 968, Appl
30	206	42.4	87	3	US-09-955-502-29	Sequence 29, Appl
31	206	42.4	87	3	US-09-955-502-30	Sequence 30, Appl
32	200	41.2	87	3	US-09-955-502-31	Sequence 31, Appl
33	200	41.2	87	3	US-09-955-502-32	Sequence 32, Appl
34	83	17.1	1647	5	US-10-450-763-41109	Sequence 41109, A
35	81	16.7	507	4	US-10-282-122A-68134	Sequence 68134, A
36	78	16.0	546	4	US-10-282-122A-66021	Sequence 66021, A
37	74.5	15.3	632	4	US-10-369-493-18744	Sequence 18744, A
38	74.5	15.3	683	6	US-11-087-099-2028	Sequence 2028, Ap
39	71.5	14.7	679	5	US-10-805-684-105	Sequence 105, App
40	71	14.6	311	5	US-10-506-454-862	Sequence 862, App
41	70.5	14.5	764	4	US-10-416-330-37	Sequence 37, Appl
42	70.5	14.5	764	5	US-10-491-467-15	Sequence 15, Appl
43	70.5	14.5	1206	5	US-10-732-923-4885	Sequence 4885, Ap
44	70.5	14.5	1206	4	US-10-085-198-144	Sequence 144, App
45	70.5	14.5	1214	5	US-10-717-665-24	Sequence 24, Appl
46	69.5	14.3	481	3	US-09-934-455-466	Sequence 466, App
47	69.5	14.3	481	4	US-10-225-066A-180	Sequence 180, App
48	69.5	14.3	481	4	US-10-225-067-64	Sequence 64, Appl
49	69.5	14.3	481	4	US-10-374-780A-396	Sequence 396, App
50	69.5	14.3	481	5	US-10-225-066A-180	Sequence 180, App
51	69.5	14.3	561	4	US-10-437-963-169643	Sequence 169643, A
52	69.5	14.3	660	6	US-11-097-143-24705	Sequence 24705, A
53	69.5	14.3	1261	4	US-10-437-963-189166	Sequence 189166, A
54	69	14.2	258	4	US-10-415-478A-36	Sequence 36, Appl
55	69	14.2	258	5	US-10-472-928-2088	Sequence 2088, Ap
56	68.5	14.1	184	4	US-10-393-840-52	Sequence 52, Appl
57	68	14.0	102	3	US-09-864-408A-768	Sequence 768, App
58	67.5	13.9	184	4	US-10-219-220-66	Sequence 66, Appl
59	67.5	13.9	184	4	US-10-393-840-118	Sequence 118, App
60	67.5	13.9	545	5	US-10-732-923-9369	Sequence 9369, Ap
61	67.5	13.9	546	3	US-09-874-923-2	Sequence 2, Appli
62	67.5	13.9	546	3	US-09-991-496-2	Sequence 2, Appli
63	67.5	13.9	546	4	US-10-098-732A-71	Sequence 71, Appl
64	67.5	13.9	926	3	US-09-991-496-128	Sequence 128, App
65	67.5	13.9	955	3	US-09-991-496-127	Sequence 127, App
66	67.5	13.9	982	3	US-09-874-923-95	Sequence 95, Appl
67	67.5	13.9	982	3	US-09-991-496-95	Sequence 95, Appl
68	67.5	13.9	1427	3	US-09-874-923-97	Sequence 97, Appl
69	67.5	13.9	1427	3	US-09-991-496-97	Sequence 97, Appl
70	67.5	13.9	1641	3	US-09-874-923-96	Sequence 96, Appl
71	67.5	13.9	1641	3	US-09-991-496-96	Sequence 96, Appl
72	67	13.8	384	6	US-11-188-298-16266	Sequence 16266, A
73	66.5	13.7	190	6	US-11-096-568A-6155	Sequence 6155, Ap
74	66.5	13.7	221	6	US-11-096-568A-6154	Sequence 6154, Ap
75	66.5	13.7	279	4	US-10-425-114-44570	Sequence 44570, A

ALIGNMENTS

RESULT 1
US-09-955-502-11
; Sequence 11, Application US/09955502
; Patent No. US20020072118A1
; GENERAL INFORMATION:
; APPLICANT: Downs, Diana M.
; APPLICANT: Gralnick, Jeff A.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; TITLE OF INVENTION: Oxygen-Labile Proteins
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955,502
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 60/234,588
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 11
; LENGTH: 91
; TYPE: PRT
; ORGANISM: Escherichia coli K-12 MG1655

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RESULT 3
US-09-955-502-13
; Sequence 13, Application US/09955502
; Patent No. US20020072118A1
; GENERAL INFORMATION:
; APPLICANT: Downs, Diana M.
; APPLICANT: Gralnack, Jeff A.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; TITLE OF INVENTION: Oxygen-Labile Proteins
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955,502
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 60/234,588
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 91
; TYPE: PRT
; ORGANISM: Escherichia coli O157:H7
US-09-955-502-13
Query Match 100.0%; Score 486; DB 3; Length 91;

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Query Match	96.5%	Score 469;	DB 3;	Length 91;
Best Local Similarity	94.5%;	Pred. No. 6.5e-45;		
Matches 86;	Conservative	5;	Mismatches 0;	Indels 0;
				Gaps 0;

Qy	1	MSRTICTFLOREAGCQDQLYPGELGKRIYNEISKEAWAOHQHQTMLINEKKNMNA	60
Db	1	MSRTICTFLQDAEQDQLYPGELGKRIYNEISKDAWAQOHQKOTMLINEKKNMNA	60
Qy	61	EHRKLEQEMVNFLEPGKEVHHIEGYTPEDKK	91
Db	61	EHRKLEQEMVNSFLPEGKDVHIEGYTPEDKK	91

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RESULT 6
US-09-955-502-17
; Sequence 17, Application US/09955502
; Patent No. US20020072118A1
; GENERAL INFORMATION:
; APPLICANT: Downs, Diana M.
; APPLICANT: Grainick, Jeff A.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; TITLE OF INVENTION: Oxygen-Labile Proteins
; FILE REFERENCE: 960296..97559
; CURRENT APPLICATION NUMBER: US/09/955,502
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 60/234,588
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 91
; TYPE: PRT
; ORGANISM: Salmonella typhi CT18
US-09-955-502-17

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```

RESULT 7
US-09-955-502-18
; Sequence 18, Application US/09955502
; Patent No. US20020072118A1
; GENERAL INFORMATION:
; APPLICANT: Downs, Diana M.
; APPLICANT: Gralnick, Jeff A.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; FILE OF INVENTION: Oxygen-Labile Proteins
; FILE REFERENCE: 960296.9/559
; CURRENT APPLICATION NUMBER: US/09/955,502
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 60/234,588
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 18
; LENGTH: 91
; TYPE: PRT
; ORGANISM: Salmonella typhimurium
US-09-955-502-18

```

Qy 61 EHRKLLLEQEMVNFLEFGKEVHIEGYTPEDKK 91
| | | | | : | | | | |
Dd 61 EHRKLLLEQEMVSFLFEGKDVIHIEGYTPEDKK 91

```

RESULT 8
US-09-955-502-15
; Sequence 15, Application US/09955502
; Patent No. US20020072118A1
; GENERAL INFORMATION:
; APPLICANT: Downs, Diana M.
; APPLICANT: Gralnick, Jeff A.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; TITLE OF INVENTION: Oxygen-Labile Proteins
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955,502
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 60/234,588
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Salmonella enteritidis
US-09-955-502-15

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RESULT 9
US-09-955-502-10
; Sequence 10, Application US/09955502
; Patent No. US20020072118A1
; GENERAL INFORMATION:
; APPLICANT: Downs, Diana M.
; APPLICANT: Gralnick, Jeff A.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; TITLE OF INVENTION: Oxygen-Labile Proteins
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955,502
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 60/234,588
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 10
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Vibrio cholerae
US-09-955-502-10

```

	Query Match	82.7%	Score 402;	DB 3;	Length 90;
	Best Local Similarity	83.3%;	Pred. No.	2.3e-37;	
	Matches .75; Conservative	7;	Mismatches	8;	Gaps 0;
Qy	1 MSRTFTFLORAEAGDFOYPGEGLGRITNEISKEAWAQWOHKQTMLINEKKLNWNA	60			
Dd	1 MARTVFCIRLQKADGIDPDIYFEEGLGRIFDNICKEAWAQWKTKQLLINEKKLNMDP	60			
Qy	61 EHRKLLEQEAMVNFFEGKEVIHGYTPEDK	90			

```
Db 61 EHRKLEQEMVNFLEFGKEVHIEGYTPPAK 90

RESULT 10
US-09-955-502-20
; Sequence 20, Application US/09955502
; Patent No. US20020072118A1
; GENERAL INFORMATION:
; APPLICANT: Downs, Diana M.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; TITLE OF INVENTION: Oxygen-Labile Proteins
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955,502
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 60/234,588
; CURRENT FILING DATE: 2000-09-22
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 20
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Yersinia pestis
US-09-955-502-20

Query Match 81.5%; Score 396; DB 3; Length 90;
Best Local Similarity 82.2%; Pred. No. 1.1e-36;
Matches 74; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

Qy 1 MSRTFCTFLQRAEGQDFQYPGELGKRIYNEISKEAWAQHQTMLINEKLLNMNA 60
Db 1 MSRTFCTFLKDAERQDFQYPGELGKRIYNEISKEAWAQHQTMLINEKLLNMNI 60

Qy 61 EHRKLEQEMVNFLEFGKEVHIEGYTPPEK 90
Db 61 EDRKLEQEMVNFLEFGQDVHIAGYTPPSK 90

RESULT 11
US-09-955-502-19
; Sequence 19, Application US/09955502
; Patent No. US20020072118A1
; GENERAL INFORMATION:
; APPLICANT: Downs, Diana M.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; TITLE OF INVENTION: Oxygen-Labile Proteins
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955,502
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 60/234,588
; CURRENT FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 19
; LENGTH: 78
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-955-502-19

Query Match 81.3%; Score 395; DB 3; Length 78;
Best Local Similarity 94.9%; Pred. No. 1.2e-36;
Matches 74; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MSRTFCTFLQRAEGQDFQYPGELGKRIYNEISKEAWAQHQTMLINEKLLNMNA 60
Db 1 MSRTFCTFLQRAEGQDFQYPGELGKRIYNEISKEAWAQHQTMLINEKLLSMNP 60

Qy 61 EHRKLEQEMVNFLEFGK 78
Db 61 EHRKLEQEMVQFLFEGK 78

RESULT 12
US-09-955-502-5
; Sequence 5, Application US/09955502
; Patent No. US20020072118A1
; GENERAL INFORMATION:
; APPLICANT: Downs, Diana M.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; TITLE OF INVENTION: Oxygen-Labile Proteins
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955,502
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 60/234,588
; CURRENT FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 5
; LENGTH: 91
; TYPE: PRT
; ORGANISM: Actinobacillus actinomycetemcomitans
US-09-955-502-5

Query Match 79.8%; Score 388; DB 3; Length 91;
Best Local Similarity 76.9%; Pred. No. 8.7e-36;
Matches 70; Conservative 11; Mismatches 10; Indels 0; Gaps 0;

Qy 1 MSRTFCTFLQRAEGQDFQYPGELGKRIYNEISKEAWAQHQTMLINEKLLNMNA 60
Db 1 MARVVFCEKLEQAEGLDFQYPGELGKRIYNEISKEAWGEMWKQTMLVNEKLLNMNA 60

Qy 61 EHRKLEQEMVNFLEFGKEVHIEGYTPPEK 91
Db 61 EHRKLEQEMVNFLEFGQDVHIEGYTPPEAK 91

RESULT 13
US-09-955-502-7
; Sequence 7, Application US/09955502
; Patent No. US20020072118A1
; GENERAL INFORMATION:
; APPLICANT: Downs, Diana M.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; TITLE OF INVENTION: Oxygen-Labile Proteins
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955,502
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 60/234,588
; CURRENT FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 7
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-09-955-502-7

Query Match 79.6%; Score 387; DB 3; Length 87;
Best Local Similarity 78.2%; Pred. No. 1.1e-35;
Matches 68; Conservative 12; Mismatches 7; Indels 0; Gaps 0;

Qy 1 MSRTFCTFLQRAEGQDFQYPGELGKRIYNEISKEAWAQHQTMLINEKLLNMNA 60
Db 1 MARTVFCEYLKKEAEGLDFQYPGELGKRIYNEISKEAWGEMWKQTMLVNEKLLNMNA 60

Qy 61 EHRKLEQEMVNFLEFGKEVHIEGYTP 87
Db 61 EHRKLEQEMVNFLEFGQDVHIEGYTP 87

RESULT 14
US-09-955-502-6
; Sequence 6, Application US/09955502
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; Patent No. US20020072118A1
; GENERAL INFORMATION:
; APPLICANT: Downs, Diana M.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955,502
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 60/234,588
; CURRENT FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Pasteurella multocida
US-09-955-502-6

Query Match      78.0%; Score 379; DB 3; Length 87;
Best Local Similarity 75.9%; Pred. No. 8.5e-35;
Matches 66; Conservative 14; Mismatches 7; Indels 0; Gaps 0;

QY 1 MGRITFCTFLQREAGQDFQLYPGELGKRIYNEISKEAWAQHQTMLINEKLLNMNA 60
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 1 MARTVFCYLLKQESGLDFQLYPGELGKRIYNEISKEAWAQHQTMLINEKLLNMNA 60
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY 61 EHRKLEQEMVNFLPEGKVEHIEGYTP 87
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 61 DHRQLEQEMVNFLPEGKDVHIEGYTP 87
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 15
US-09-955-502-8
; Sequence 8, Application US/09955502
; Patent No. US20020072118A1
; GENERAL INFORMATION:
; APPLICANT: Downs, Diana M.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955,502
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 60/234,588
; CURRENT FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Haemophilus ducreyi
US-09-955-502-8

Query Match      76.7%; Score 373; DB 3; Length 87;
Best Local Similarity 75.9%; Pred. No. 4.1e-34;
Matches 66; Conservative 12; Mismatches 9; Indels 0; Gaps 0;

QY 1 MGRITFCTFLQREAGQDFQLYPGELGKRIYNEISKEAWAQHQTMLINEKLLNMNA 60
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 1 MARMVFCYLLKQESGLDFQLYPGELGKRIYNEISKEAWAQHQTMLINEKLLNMNP 60
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY 61 EHRKLEQEMVNFLPEGKVEHIEGYTP 87
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 61 EHRQLEQEMVNFLPEGKDVHIDGYTP 87
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 16
US-09-955-502-9
; Sequence 9, Application US/09955502
; Patent No. US20020072118A1
; GENERAL INFORMATION:
; APPLICANT: Downs, Diana M.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955,502
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 60/234,588
; CURRENT FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Shewanella putrefasciens
US-09-955-502-9

Query Match      68.3%; Score 332; DB 3; Length 88;
Best Local Similarity 68.2%; Pred. No. 1.7e-29;
Matches 60; Conservative 12; Mismatches 16; Indels 0; Gaps 0;

QY 1 MGRITFCTFLQREAGQDFQLYPGELGKRIYNEISKEAWAQHQTMLINEKLLNMNA 60
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 1 MARTVNCVHLNKEADGLDFQLYPGDLGKRIYNEISKEAWGLWQKQTMLINEKLLNMNV 60
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY 61 EHRKLEQEMVNFLPEGKVEHIEGYTP 88
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 61 DDRKLEAQMTSFLPEGKDVIEGYTP 88
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 17
US-09-955-502-21
; Sequence 21, Application US/09955502
; Patent No. US20020072118A1
; GENERAL INFORMATION:
; APPLICANT: Downs, Diana M.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955,502
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 60/234,588
; CURRENT FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Buchnera sp. APS
US-09-955-502-21

Query Match      54.5%; Score 265; DB 3; Length 76;
Best Local Similarity 61.8%; Pred. No. 5.1e-22;
Matches 47; Conservative 16; Mismatches 13; Indels 0; Gaps 0;

QY 1 MGRITFCTFLQREAGQDFQLYPGELGKRIYNEISKEAWAQHQTMLINEKLLNMNA 60
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 1 MARIIFCTFFKKSEQDFQSYPGKLGKIIYDQSKKAWEKWIKQTLINENLNMFNL 60
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY 61 EHRKLEQEMVNFLPE 76
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 61 EHRKKIEKYMKLFLPK 76
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 18
US-09-955-502-2
; Sequence 2, Application US/09955502
; Patent No. US20020072118A1
; GENERAL INFORMATION:
; APPLICANT: Downs, Diana M.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955,502
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 60/234,588
; CURRENT FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Buchnera sp. APS
US-09-955-502-21
```



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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Coxiella burnetii
US-09-955-502-33

Query Match
Best Local Similarity 46.7%; Score 227; DB 3; Length 88;
Matches 44; Conservative 16; Mismatches 28; Indels 0; Gaps 0;

QY 1 MGRITCTFLQREAGQDFQLYPGELGKRIYNEISKEAWAQHQTMLINEKLLNMNA 60
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 1 MTRRIICQKLGKDALNYPYPGELGERIYNHISEQAWQALSHQTMLINEYRLSLIDP 60
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 61 EHRKLEQEMVNFLEPGKEVHIEGYTPE 88
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 61 KARQFLEQEMINFLFGTSEKPAQITSE 88
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 23
US-09-955-502-23
; Sequence 23, Application US/09955502
; Patent No. US20020072118A1
; GENERAL INFORMATION:
; APPLICANT: Downs, Diana M.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; TITLE OF INVENTION: Oxygen-Labile Proteins
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955,502
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 60/234,588
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Pseudomonas syringae
US-09-955-502-23

Query Match
Best Local Similarity 46.7%; Score 227; DB 3; Length 90;
Matches 43; Conservative 15; Mismatches 32; Indels 0; Gaps 0;

QY 1 MGRITCTFLQREAGQDFQLYPGELGKRIYNEISKEAWAQHQTMLINEKLLNMNA 60
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 1 MTRTWCRKYKEELPGLERAPYPGAKGEDIFNHVSQKAWADWQKHQTMLINERRLLNMNA 60
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 61 EHRKLEQEMVNFLEPGKEVHIEGYTPEDK 90
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 61 EDRKFLQEMDKFLSGEYQAQAEQVPPPK 90
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 24
US-09-955-502-22
; Sequence 22, Application US/09955502
; Patent No. US20020072118A1
; GENERAL INFORMATION:
; APPLICANT: Downs, Diana M.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; TITLE OF INVENTION: Oxygen-Labile Proteins
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955,502
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 60/234,588
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Xylella fastidiosa
US-09-955-502-22

Query Match
Best Local Similarity 46.5%; Score 226; DB 3; Length 89;
Matches 45; Conservative 10; Mismatches 34; Indels 0; Gaps 0;

QY 1 MGRITCTFLQREAGQDFQLYPGELGKRIYNEISKEAWAQHQTMLINEKLLNMNA 60
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 1 MQRITCEYEQRDTEGLDFVYPGELGQKIFACIGKVGWAAWLHQHQTMLINENRISPRNP 60
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 61 EHRKLEQEMVNFLEPGKEVHIEGYTPE 89
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 61 SHRAFLEELNKFLEPERRVAKPEGYIEPD 89
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 25
US-09-955-502-24
; Sequence 24, Application US/09955502
; Patent No. US20020072118A1
; GENERAL INFORMATION:
; APPLICANT: Downs, Diana M.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; TITLE OF INVENTION: Oxygen-Labile Proteins
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955,502
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 60/234,588
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Pseudomonas putida
US-09-955-502-24

Query Match
Best Local Similarity 46.3%; Score 225; DB 3; Length 87;
Matches 47; Conservative 10; Mismatches 29; Indels 2; Gaps 2;

QY 1 MGRITCTFLQREAGQDFQLYPGELGKRIYNEISKEAWAQHQTMLINEKLLNMNA 60
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 1 MTRTWCRKYQBELPGLERPPYPGAKGQDIFEHISQKAWADWQKHQTMLINEKLLNMNA 60
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 61 EHRKLEQEMVNFLEPGKE-VHIEGYTP 87
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 61 EDRKFLQAEWDKF-PAGEEYQAQAEQVYP 87
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

Search completed: June 27, 2007, 11:29:08
Job time : 188 secs
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GenCore version 6.2.1
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OM protein - protein search, using sw model

Run on: June 27, 2007, 11:26:12 ; Search time 141 Seconds
(without alignments)
221.752 Million cell updates/sec

Title: US-09-955-502a-11
Perfect score: 486
Sequence: 1 MSRTICTFLQREAGQDFQ.....NFLFEGKEVHIEGYTPEDKK 91

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1408788 seqs, 343594471 residues

Total number of hits satisfying chosen parameters: 1408788

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

Database : Published Applications AA New.*

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2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pap.*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pap.*
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6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pap.*
7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pap.*
8: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	231	47.5	122	6	US-10-419-128-23355
2	131	27.0	110	6	US-10-603-108-2859
3	85.5	17.6	514	7	US-11-516-230-44315
4	81	16.7	507	7	US-11-516-230-44283
5	81	16.7	508	7	US-11-516-230-44299
6	78	16.0	507	7	US-11-516-230-44263
7	78	16.0	546	7	US-11-516-230-44265
8	75.5	15.5	507	7	US-11-516-230-44271
9	75	15.4	309	6	US-10-526-324-706
10	72	14.8	474	6	US-10-419-128-24473
11	72	14.8	507	7	US-11-516-230-44261
12	71.5	14.7	118	6	US-10-703-032-118890
13	71.5	14.7	566	6	US-10-276-8178-12931
14	70.5	14.5	285	6	US-10-917-503-11063
15	70.5	14.5	313	7	US-11-443-428A-90387
16	70.5	14.5	313	7	US-11-443-428A-90388
17	70.5	14.5	614	6	US-10-567-867-1402
18	70.5	14.5	647	7	US-11-443-428A-890383
19	70.5	14.5	702	6	US-10-405-027-3329
20	70.5	14.5	764	7	US-11-582-861-6676
21	70.5	14.5	995	7	US-11-582-861-6675
22	70.5	14.5	1072	7	US-11-443-428A-890379
23	70.5	14.5	1072	7	US-11-443-428A-890395
24	70.5	14.5	1107	7	US-11-443-428A-890399
25	70.5	14.5	1115	7	US-11-443-428A-890396

ALIGNMENTS

RESULT 1

US-10-419-128-23355
; Sequence 23355, Application US/10419128
; Publication No. US20070020624A1
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/10/419,128
; CURRENT FILING DATE: 2003-04-21
; PRIOR APPLICATION NUMBER: US/09/252,991
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142

26	70.5	14.5	1125	7	US-11-443-428A-890402	Sequence 890402,
27	70.5	14.5	1135	7	US-11-443-428A-890378	Sequence 890378,
28	70.5	14.5	1135	7	US-11-443-428A-890392	Sequence 890392,
29	70.5	14.5	1140	7	US-11-443-428A-890382	Sequence 890382,
30	70.5	14.5	1140	7	US-11-443-428A-890394	Sequence 890394,
31	70.5	14.5	1142	7	US-11-443-428A-890386	Sequence 890386,
32	70.5	14.5	1143	7	US-11-443-428A-890390	Sequence 890390,
33	70.5	14.5	1159	7	US-11-443-428A-890381	Sequence 890381,
34	70.5	14.5	1160	7	US-11-443-428A-890393	Sequence 890393,
35	70.5	14.5	1170	7	US-11-443-428A-890398	Sequence 890398,
36	70.5	14.5	1180	7	US-11-582-861-6674	Sequence 6674, Ap
37	70.5	14.5	1186	7	US-11-443-428A-890384	Sequence 890384,
38	70.5	14.5	1186	7	US-11-582-861-6672	Sequence 6672, Ap
39	70.5	14.5	1188	7	US-11-443-428A-890397	Sequence 890397,
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41	70.5	14.5	1196	7	US-11-443-428A-890380	Sequence 890380,
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43	69.5	14.3	374	7	US-11-443-428A-861008	Sequence 861008,
44	69.5	14.3	395	7	US-11-443-428A-861006	Sequence 861006,
45	69.5	14.3	456	7	US-11-443-428A-861004	Sequence 861004,
46	69.5	14.3	481	6	US-10-374-780A-396	Sequence 396, App
47	69.5	14.3	481	7	US-11-375-241-64	Sequence 375, App
48	69.5	14.3	488	6	US-10-917-503-15108	Sequence 15108, A
49	69.5	14.3	488	7	US-11-371-354-74169	Sequence 74169, A
50	69.5	14.3	488	7	US-11-443-428A-861002	Sequence 861002,
51	69.5	14.3	498	7	US-11-443-428A-861012	Sequence 861012,
52	69.5	14.3	498	7	US-11-443-428A-861005	Sequence 861005,
53	69.5	14.3	507	7	US-11-516-230-44365	Sequence 44365, A
54	69.5	14.3	511	7	US-11-443-428A-861009	Sequence 861009,
55	69.5	14.3	529	7	US-11-443-428A-861010	Sequence 861010,
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60	68.5	14.1	509	7	US-11-516-230-44341	Sequence 44341, A
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63	68	14.0	164	7	US-11-443-428A-919650	Sequence 919650,
64	68	14.0	213	6	US-10-467-478-806	Sequence 806, App
65	68	14.0	473	6	US-10-474-894-15	Sequence 15, Appl
66	68	14.0	473	6	US-10-760-320A-2528	Sequence 2528, Ap
67	68	14.0	473	7	US-11-582-861-7080	Sequence 7080, Ap
68	68	14.0	2951	6	US-10-467-478-814	Sequence 814, App
69	68	14.0	4560	6	US-10-467-478-551	Sequence 551, App
70	67.5	13.9	1131	7	US-11-330-403-983	Sequence 983, App
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72	67	13.8	79	7	US-11-443-428A-965050	Sequence 965050,
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; PRIOR APPLICATION NUMBER: EP 06110579.7
; PRIOR FILING DATE: 2006-02-28
; PRIOR APPLICATION NUMBER: EP 06110425.3
; PRIOR FILING DATE: 2006-02-24
; PRIOR APPLICATION NUMBER: EP 06110423.8
; PRIOR FILING DATE: 2006-02-24
; PRIOR APPLICATION NUMBER: EP 06110418.8
; PRIOR FILING DATE: 2006-02-24
; PRIOR APPLICATION NUMBER: EP 06110383.4
; PRIOR FILING DATE: 2006-02-24
; PRIOR APPLICATION NUMBER: EP 06110378.4
; PRIOR FILING DATE: 2006-02-24
; PRIOR APPLICATION NUMBER: EP 06110367.7
; PRIOR FILING DATE: 2006-02-24
; PRIOR APPLICATION NUMBER: EP 06110327.1
; PRIOR FILING DATE: 2006-02-23
; PRIOR APPLICATION NUMBER: EP 06110325.5
; PRIOR FILING DATE: 2006-02-23
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 73449
; SOFTWARE: Biomat PatentTool according to PatentIn 3.1 format
; SEQ ID NO 44315
; LENGTH: 514
; TYPE: PRT
; ORGANISM: Desulfotalea psychrophila LSV54
US-11-516-230-44315

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RESULT 4
US-11-516-230-44283
; Sequence 44283, Application US/11516230
; Publication No. US20070118916A1
; GENERAL INFORMATION:
; APPLICANT: Plesch, Gunnar
; APPLICANT: Puzio, Piotr
; APPLICANT: Blau, Astrid
; APPLICANT: Herold, Manfred
; APPLICANT: Wendel, Birgit
; APPLICANT: Kamlage, Beate
; APPLICANT: Schauwecker, Florian
; APPLICANT: Looser, Ralf
; TITLE OF INVENTION: Process for the production of fine chemicals
; FILE REFERENCE: 13195-00014-US
; CURRENT APPLICATION NUMBER: US/11/516,230
; CURRENT FILING DATE: 2006-09-06
; PRIOR APPLICATION NUMBER: EP 06110426.1
; PRIOR FILING DATE: 2006-02-24
; PRIOR APPLICATION NUMBER: EP 06110579.7
; PRIOR FILING DATE: 2006-02-28
; PRIOR APPLICATION NUMBER: EP 06110425.3
; PRIOR FILING DATE: 2006-02-24
; PRIOR APPLICATION NUMBER: EP 06110423.8
; PRIOR FILING DATE: 2006-02-24
; PRIOR APPLICATION NUMBER: EP 06110418.8
; PRIOR FILING DATE: 2006-02-24
; PRIOR APPLICATION NUMBER: EP 06110383.4
; PRIOR FILING DATE: 2006-02-24
; PRIOR APPLICATION NUMBER: EP 06110378.4
; PRIOR FILING DATE: 2006-02-24
; PRIOR APPLICATION NUMBER: EP 06110367.7
; PRIOR FILING DATE: 2006-02-24
; PRIOR APPLICATION NUMBER: EP 06110327.1
; PRIOR FILING DATE: 2006-02-23
; PRIOR APPLICATION NUMBER: EP 06110325.5
; PRIOR FILING DATE: 2006-02-23

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; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 73449
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; SEQ ID NO 44283
; LENGTH: 507
; TYPE: PRT
; ORGANISM: Pseudomonas putida KT2440
US-11-516-230-44283

Query Match      16.7%; Score 81; DB 7; Length 507;
Best Local Similarity 28.2%; Pred. No. 6.3;
Matches 22; Conservative 16; Mismatches 28; Indels 12; Gaps 3;

QY 13 EAEQDQFLYP-----GELGKRI-YNEISKEAWAQWQHKTMLINEKLNMMNAEHRKL 65
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QY 66 LEQEMVNFLEGEVHIE 83
Db 353 ----MVEMLNRGEELPVD 366

RESULT 5
US-11-516-230-44299
; Sequence 44299, Application US/11516230
; Publication No. US20070118916A1
; GENERAL INFORMATION:
; APPLICANT: Plesch, Gunnar
; APPLICANT: Puzio, Piotr
; APPLICANT: Blau, Astrid
; APPLICANT: Herold, Manfred
; APPLICANT: Wendel, Birgit
; APPLICANT: Kamlage, Beate
; APPLICANT: Schauwecker, Florian
; APPLICANT: Looser, Ralf
; TITLE OF INVENTION: Process for the production of fine chemicals
; FILE REFERENCE: 13195-00014-US
; CURRENT APPLICATION NUMBER: US/11/516,230
; CURRENT FILING DATE: 2006-09-06
; PRIOR APPLICATION NUMBER: EP 06110426.1
; PRIOR FILING DATE: 2006-02-24
; PRIOR APPLICATION NUMBER: EP 06110579.7
; PRIOR FILING DATE: 2006-02-28
; PRIOR APPLICATION NUMBER: EP 06110425.3
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; PRIOR APPLICATION NUMBER: EP 06110418.8
; PRIOR FILING DATE: 2006-02-24
; PRIOR APPLICATION NUMBER: EP 06110383.4
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; PRIOR APPLICATION NUMBER: EP 06110378.4
; PRIOR FILING DATE: 2006-02-24
; PRIOR APPLICATION NUMBER: EP 06110367.7
; PRIOR FILING DATE: 2006-02-24
; PRIOR APPLICATION NUMBER: EP 06110327.1
; PRIOR FILING DATE: 2006-02-23
; PRIOR APPLICATION NUMBER: EP 06110325.5
; PRIOR FILING DATE: 2006-02-23
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 73449
; SOFTWARE: Biomax PatentTool according to PatentIN 3.1 format
; SEQ ID NO 44299
; LENGTH: 508
; TYPE: PRT
; ORGANISM: Chromobacterium violaceum ATCC 12472
US-11-516-230-44299

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Best Local Similarity 30.2%; Pred. No. 6.3;
Matches 19; Conservative 17; Mismatches 21; Indels 6; Gaps 2;

QY 22 YPGELGKRI-YNEISKEAWAQWQHKTMLINEKLNMMNAEHRKLLEQEMVNFLEGEV 80
Db 294 ELEAPSLDAYPIVWEAGPSARRVLLDITPEVASWKPGETILLNGKMLTGRDAHKKR- 352
QY 66 LEQEMVNFLEGEVHIE 83
Db 353 ----MVEMLNRGEELPVD 366

RESULT 6
US-11-516-230-44263
; Sequence 44263, Application US/11516230
; Publication No. US20070118916A1
; GENERAL INFORMATION:
; APPLICANT: Plesch, Gunnar
; APPLICANT: Puzio, Piotr
; APPLICANT: Blau, Astrid
; APPLICANT: Herold, Manfred
; APPLICANT: Wendel, Birgit
; APPLICANT: Kamlage, Beate
; APPLICANT: Schauwecker, Florian
; APPLICANT: Looser, Ralf
; TITLE OF INVENTION: Process for the production of fine chemicals
; FILE REFERENCE: 13195-00014-US
; CURRENT APPLICATION NUMBER: US/11/516,230
; CURRENT FILING DATE: 2006-09-06
; PRIOR APPLICATION NUMBER: EP 06110426.1
; PRIOR FILING DATE: 2006-02-24
; PRIOR APPLICATION NUMBER: EP 06110579.7
; PRIOR FILING DATE: 2006-02-28
; PRIOR APPLICATION NUMBER: EP 06110425.3
; PRIOR FILING DATE: 2006-02-24
; PRIOR APPLICATION NUMBER: EP 06110423.8
; PRIOR FILING DATE: 2006-02-24
; PRIOR APPLICATION NUMBER: EP 06110418.8
; PRIOR FILING DATE: 2006-02-24
; PRIOR APPLICATION NUMBER: EP 06110383.4
; PRIOR FILING DATE: 2006-02-24
; PRIOR APPLICATION NUMBER: EP 06110378.4
; PRIOR FILING DATE: 2006-02-24
; PRIOR APPLICATION NUMBER: EP 06110367.7
; PRIOR FILING DATE: 2006-02-24
; PRIOR APPLICATION NUMBER: EP 06110327.1
; PRIOR FILING DATE: 2006-02-23
; PRIOR APPLICATION NUMBER: EP 06110325.5
; PRIOR FILING DATE: 2006-02-23
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 73449
; SOFTWARE: Biomax PatentTool according to PatentIN 3.1 format
; SEQ ID NO 44263
; LENGTH: 507
; TYPE: PRT
; ORGANISM: Neisseria meningitidis MC58
US-11-516-230-44263

Query Match      16.0%; Score 78; DB 7; Length 507;
Best Local Similarity 30.2%; Pred. No. 13;
Matches 19; Conservative 18; Mismatches 20; Indels 6; Gaps 2;

QY 22 YPGELGKRI-YNEISKEAWAQWQHKTMLINEKLNMMNAEHRKLLEQEMVNFLEGEV 80
Db 294 ELEAPSLDAYPIVWEAGPSARRVLLDITPEVASWKPGETILLNGKMLTGRDAHKKR- 352
QY 66 LEQEMVNFLEGEVHIE 83
Db 366 PVD 368

RESULT 7
US-11-516-230-44265
; Sequence 44265, Application US/11516230
; Publication No. US20070118916A1
; GENERAL INFORMATION:
; APPLICANT: Plesch, Gunnar
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; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 73449
; SOFTWARE: Biomax PatentTool according to PatentIN 3.1 format
; SEQ ID NO 44283
; LENGTH: 507
; TYPE: PRT
; ORGANISM: Pseudomonas putida KT2440
US-11-516-230-44283

Query Match      16.7%; Score 81; DB 7; Length 507;
Best Local Similarity 28.2%; Pred. No. 6.3;
Matches 22; Conservative 16; Mismatches 28; Indels 12; Gaps 3;

QY 13 EAEQDQFLYP-----GELGKRI-YNEISKEAWAQWQHKTMLINEKLNMMNAEHRKL 65
Db 294 ELEAPSLDAYPIVWEAGPSARRVLLDITPEVASWKPGETILLNGKMLTGRDAHKKR- 352
QY 66 LEQEMVNFLEGEVHIE 83
Db 353 ----MVEMLNRGEELPVD 366

RESULT 5
US-11-516-230-44299
; Sequence 44299, Application US/11516230
; Publication No. US20070118916A1
; GENERAL INFORMATION:
; APPLICANT: Plesch, Gunnar
; APPLICANT: Puzio, Piotr
; APPLICANT: Blau, Astrid
; APPLICANT: Herold, Manfred
; APPLICANT: Wendel, Birgit
; APPLICANT: Kamlage, Beate
; APPLICANT: Schauwecker, Florian
; APPLICANT: Looser, Ralf
; TITLE OF INVENTION: Process for the production of fine chemicals
; FILE REFERENCE: 13195-00014-US
; CURRENT APPLICATION NUMBER: US/11/516,230
; CURRENT FILING DATE: 2006-09-06
; PRIOR APPLICATION NUMBER: EP 06110426.1
; PRIOR FILING DATE: 2006-02-24
; PRIOR APPLICATION NUMBER: EP 06110579.7
; PRIOR FILING DATE: 2006-02-28
; PRIOR APPLICATION NUMBER: EP 06110425.3
; PRIOR FILING DATE: 2006-02-24
; PRIOR APPLICATION NUMBER: EP 06110423.8
; PRIOR FILING DATE: 2006-02-24
; PRIOR APPLICATION NUMBER: EP 06110418.8
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; PRIOR APPLICATION NUMBER: EP 06110383.4
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; PRIOR APPLICATION NUMBER: EP 06110378.4
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; PRIOR APPLICATION NUMBER: EP 06110367.7
; PRIOR FILING DATE: 2006-02-24
; PRIOR APPLICATION NUMBER: EP 06110327.1
; PRIOR FILING DATE: 2006-02-23
; PRIOR APPLICATION NUMBER: EP 06110325.5
; PRIOR FILING DATE: 2006-02-23
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 73449
; SOFTWARE: Biomax PatentTool according to PatentIN 3.1 format
; SEQ ID NO 44299
; LENGTH: 508
; TYPE: PRT
; ORGANISM: Chromobacterium violaceum ATCC 12472
US-11-516-230-44299

Query Match      16.7%; Score 81; DB 7; Length 508;
Best Local Similarity 30.2%; Pred. No. 6.3;
Matches 19; Conservative 17; Mismatches 21; Indels 6; Gaps 2;

QY 22 YPGELGKRI-YNEISKEAWAQWQHKTMLINEKLNMMNAEHRKLLEQEMVNFLEGEV 80
Db 294 ELEAPSLDAYPIVWEAGPSARRVLLDITPEVASWKPGETILLNGKMLTGRDAHKKR- 352
QY 66 LEQEMVNFLEGEVHIE 83
Db 353 ----MVEMLNRGEELPVD 366

RESULT 6
US-11-516-230-44263
; Sequence 44263, Application US/11516230
; Publication No. US20070118916A1
; GENERAL INFORMATION:
; APPLICANT: Plesch, Gunnar
; APPLICANT: Puzio, Piotr
; APPLICANT: Blau, Astrid
; APPLICANT: Herold, Manfred
; APPLICANT: Wendel, Birgit
; APPLICANT: Kamlage, Beate
; APPLICANT: Schauwecker, Florian
; APPLICANT: Looser, Ralf
; TITLE OF INVENTION: Process for the production of fine chemicals
; FILE REFERENCE: 13195-00014-US
; CURRENT APPLICATION NUMBER: US/11/516,230
; CURRENT FILING DATE: 2006-09-06
; PRIOR APPLICATION NUMBER: EP 06110426.1
; PRIOR FILING DATE: 2006-02-24
; PRIOR APPLICATION NUMBER: EP 06110579.7
; PRIOR FILING DATE: 2006-02-28
; PRIOR APPLICATION NUMBER: EP 06110425.3
; PRIOR FILING DATE: 2006-02-24
; PRIOR APPLICATION NUMBER: EP 06110423.8
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; PRIOR APPLICATION NUMBER: EP 06110418.8
; PRIOR FILING DATE: 2006-02-24
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; PRIOR FILING DATE: 2006-02-24
; PRIOR APPLICATION NUMBER: EP 06110378.4
; PRIOR FILING DATE: 2006-02-24
; PRIOR APPLICATION NUMBER: EP 06110367.7
; PRIOR FILING DATE: 2006-02-24
; PRIOR APPLICATION NUMBER: EP 06110327.1
; PRIOR FILING DATE: 2006-02-23
; PRIOR APPLICATION NUMBER: EP 06110325.5
; PRIOR FILING DATE: 2006-02-23
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 73449
; SOFTWARE: Biomax PatentTool according to PatentIN 3.1 format
; SEQ ID NO 44263
; LENGTH: 507
; TYPE: PRT
; ORGANISM: Neisseria meningitidis MC58
US-11-516-230-44263

Query Match      16.0%; Score 78; DB 7; Length 507;
Best Local Similarity 30.2%; Pred. No. 13;
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QY 22 YPGELGKRI-YNEISKEAWAQWQHKTMLINEKLNMMNAEHRKLLEQEMVNFLEGEV 80
Db 294 ELEAPSLDAYPIVWEAGPSARRVLLDITPEVASWKPGETILLNGKMLTGRDAHKKR- 352
QY 66 LEQEMVNFLEGEVHIE 83
Db 366 PVD 368

RESULT 7
US-11-516-230-44265
; Sequence 44265, Application US/11516230
; Publication No. US20070118916A1
; GENERAL INFORMATION:
; APPLICANT: Plesch, Gunnar
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; APPLICANT: Puzio, Piotr
; APPLICANT: Blau, Astrid
; APPLICANT: Herold, Manfred
; APPLICANT: Wendel, Birgit
; APPLICANT: Kamlage, Beate
; APPLICANT: Schaecker, Florian
; APPLICANT: Looser, Ralf
; TITLE OF INVENTION: Process for the production of fine chemicals
; FILE REFERENCE: 13195-00014-US
; CURRENT APPLICATION NUMBER: US/11/516,230
; CURRENT FILING DATE: 2006-09-06
; PRIOR FILING DATE: 2006-02-24
; PRIOR APPLICATION NUMBER: EP 06110426.1
; PRIOR FILING DATE: 2006-02-24
; PRIOR APPLICATION NUMBER: EP 06110579.7
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; PRIOR APPLICATION NUMBER: EP 06110425.3
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; PRIOR FILING DATE: 2006-02-24
; PRIOR APPLICATION NUMBER: EP 06110367.7
; PRIOR FILING DATE: 2006-02-23
; PRIOR APPLICATION NUMBER: EP 06110327.1
; PRIOR FILING DATE: 2006-02-23
; PRIOR APPLICATION NUMBER: EP 06110325.5
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 73449
; SOFTWARE: Biomax PatentTool according to PatentIN 3.1 format
; SEQ ID NO 44265
; LENGTH: 546
; TYPE: PR1
; ORGANISM: Neisseria meningitidis Z2491
US-11-516-230-44265

Query Match      16.0%; Score 78; DB 7; Length 546;
Best Local Similarity 30.2%; Pred.No. 14;
Matches 19; Conservative 18; Mismatches 20; Indels 6; Gaps 2;

QY    22 YPGLGKRI-YNEISKEAWAQHQTMLINEKKLNMMNAHRKLLEQWVNFPEGEKV 80
Db    350 YSPDNGKRVDVKLTKEEVASWKTDGVLLNGKILTGRTDAHKRL-----VDMLDKGEEEL 404
QY    81 HIE 83
Db    405 PVD 407

RESULT 8
US-11-516-230-44271
; Sequence 44271, Application US/11516230
; Publication No. US20070118916A1
; GENERAL INFORMATION:
; APPLICANT: Plesch, Gunnar
; APPLICANT: Puzio, Piotr
; APPLICANT: Blau, Astrid
; APPLICANT: Herold, Manfred
; APPLICANT: Wendel, Birgit
; APPLICANT: Kamlage, Beate
; APPLICANT: Schaecker, Florian
; APPLICANT: Looser, Ralf
; TITLE OF INVENTION: Process for the production of fine chemicals
; FILE REFERENCE: 13195-00014-US
; CURRENT APPLICATION NUMBER: US/11/516,230
; CURRENT FILING DATE: 2006-09-06
; PRIOR APPLICATION NUMBER: EP 06110426.1
; PRIOR FILING DATE: 2006-02-24
; PRIOR APPLICATION NUMBER: EP 06110579.7
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 73449
; SOFTWARE: Biomax PatentTool according to PatentIN 3.1 format
; SEQ ID NO 44265
; LENGTH: 546
; TYPE: PR1
; ORGANISM: Neisseria meningitidis Z2491
US-11-516-230-44265

Query Match      16.0%; Score 78; DB 7; Length 546;
Best Local Similarity 30.2%; Pred.No. 14;
Matches 19; Conservative 18; Mismatches 20; Indels 6; Gaps 2;

QY    22 YPGLGKRI-YNEISKEAWAQHQTMLINEKKLNMMNAHRKLLEQWVNFPEGEKV 80
Db    350 YSPDNGKRVDVKLTKEEVASWKTDGVLLNGKILTGRTDAHKRL-----VDMLDKGEEEL 404
QY    81 HIE 83
Db    405 PVD 407

RESULT 8
US-11-516-230-44271
; Sequence 44271, Application US/11516230
; Publication No. US20070118916A1
; GENERAL INFORMATION:
; APPLICANT: Plesch, Gunnar
; APPLICANT: Puzio, Piotr
; APPLICANT: Blau, Astrid
; APPLICANT: Herold, Manfred
; APPLICANT: Wendel, Birgit
; APPLICANT: Kamlage, Beate
; APPLICANT: Schaecker, Florian
; APPLICANT: Looser, Ralf
; TITLE OF INVENTION: Process for the production of fine chemicals
; FILE REFERENCE: 13195-00014-US
; CURRENT APPLICATION NUMBER: US/11/516,230
; CURRENT FILING DATE: 2006-09-06
; PRIOR APPLICATION NUMBER: EP 06110426.1
; PRIOR FILING DATE: 2006-02-24
; PRIOR APPLICATION NUMBER: EP 06110579.7
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 73449
; SOFTWARE: Biomax PatentTool according to PatentIN 3.1 format
; SEQ ID NO 44265
; LENGTH: 546
; TYPE: PR1
; ORGANISM: Neisseria meningitidis Z2491
US-11-516-230-44265

Query Match      16.0%; Score 78; DB 7; Length 546;
Best Local Similarity 30.2%; Pred.No. 14;
Matches 19; Conservative 18; Mismatches 20; Indels 6; Gaps 2;

QY    22 YPGLGKRI-YNEISKEAWAQHQTMLINEKKLNMMNAHRKLLEQWVNFPEGEKV 80
Db    350 YSPDNGKRVDVKLTKEEVASWKTDGVLLNGKILTGRTDAHKRL-----VDMLDKGEEEL 404
QY    81 HIE 83
Db    405 PVD 407

RESULT 8
US-11-516-230-44271
; Sequence 44271, Application US/11516230
; Publication No. US20070118916A1
; GENERAL INFORMATION:
; APPLICANT: Plesch, Gunnar
; APPLICANT: Puzio, Piotr
; APPLICANT: Blau, Astrid
; APPLICANT: Herold, Manfred
; APPLICANT: Wendel, Birgit
; APPLICANT: Kamlage, Beate
; APPLICANT: Schaecker, Florian
; APPLICANT: Looser, Ralf
; TITLE OF INVENTION: Process for the production of fine chemicals
; FILE REFERENCE: 13195-00014-US
; CURRENT APPLICATION NUMBER: US/11/516,230
; CURRENT FILING DATE: 2006-09-06
; PRIOR APPLICATION NUMBER: EP 06110426.1
; PRIOR FILING DATE: 2006-02-24
; PRIOR APPLICATION NUMBER: EP 06110579.7
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 73449
; SOFTWARE: Biomax PatentTool according to PatentIN 3.1 format
; SEQ ID NO 44265
; LENGTH: 546
; TYPE: PR1
; ORGANISM: Neisseria meningitidis Z2491
US-11-516-230-44265

Query Match      16.0%; Score 78; DB 7; Length 546;
Best Local Similarity 30.2%; Pred.No. 14;
Matches 19; Conservative 18; Mismatches 20; Indels 6; Gaps 2;

QY    22 YPGLGKRI-YNEISKEAWAQHQTMLINEKKLNMMNAHRKLLEQWVNFPEGEKV 80
Db    350 YSPDNGKRVDVKLTKEEVASWKTDGVLLNGKILTGRTDAHKRL-----VDMLDKGEEEL 404
QY    81 HIE 83
Db    405 PVD 407

RESULT 8
US-11-516-230-44271
; Sequence 44271, Application US/11516230
; Publication No. US20070118916A1
; GENERAL INFORMATION:
; APPLICANT: Plesch, Gunnar
; APPLICANT: Puzio, Piotr
; APPLICANT: Blau, Astrid
; APPLICANT: Herold, Manfred
; APPLICANT: Wendel, Birgit
; APPLICANT: Kamlage, Beate
; APPLICANT: Schaecker, Florian
; APPLICANT: Looser, Ralf
; TITLE OF INVENTION: Process for the production of fine chemicals
; FILE REFERENCE: 13195-00014-US
; CURRENT APPLICATION NUMBER: US/11/516,230
; CURRENT FILING DATE: 2006-09-06
; PRIOR APPLICATION NUMBER: EP 06110426.1
; PRIOR FILING DATE: 2006-02-24
; PRIOR APPLICATION NUMBER: EP 06110579.7
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 73449
; SOFTWARE: Biomax PatentTool according to PatentIN 3.1 format
; SEQ ID NO 44265
; LENGTH: 546
; TYPE: PR1
; ORGANISM: Neisseria meningitidis Z2491
US-11-516-230-44265

Query Match      16.0%; Score 78; DB 7; Length 546;
Best Local Similarity 30.2%; Pred.No. 14;
Matches 19; Conservative 18; Mismatches 20; Indels 6; Gaps 2;

QY    22 YPGLGKRI-YNEISKEAWAQHQTMLINEKKLNMMNAHRKLLEQWVNFPEGEKV 80
Db    350 YSPDNGKRVDVKLTKEEVASWKTDGVLLNGKILTGRTDAHKRL-----VDMLDKGEEEL 404
QY    81 HIE 83
Db    405 PVD 407

RESULT 8
US-11-516-230-44271
; Sequence 44271, Application US/11516230
; Publication No. US20070118916A1
; GENERAL INFORMATION:
; APPLICANT: Plesch, Gunnar
; APPLICANT: Puzio, Piotr
; APPLICANT: Blau, Astrid
; APPLICANT: Herold, Manfred
; APPLICANT: Wendel, Birgit
; APPLICANT: Kamlage, Beate
; APPLICANT: Schaecker, Florian
; APPLICANT: Looser, Ralf
; TITLE OF INVENTION: Process for the production of fine chemicals
; FILE REFERENCE: 13195-00014-US
; CURRENT APPLICATION NUMBER: US/11/516,230
; CURRENT FILING DATE: 2006-09-06
; PRIOR APPLICATION NUMBER: EP 06110426.1
; PRIOR FILING DATE: 2006-02-24
; PRIOR APPLICATION NUMBER: EP 06110579.7
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 73449
; SOFTWARE: Biomax PatentTool according to PatentIN 3.1 format
; SEQ ID NO 44265
; LENGTH: 546
; TYPE: PR1
; ORGANISM: Neisseria meningitidis Z2491
US-11-516-230-44265

Query Match      16.0%; Score 78; DB 7; Length 546;
Best Local Similarity 30.2%; Pred.No. 14;
Matches 19; Conservative 18; Mismatches 20; Indels 6; Gaps 2;

QY    22 YPGLGKRI-YNEISKEAWAQHQTMLINEKKLNMMNAHRKLLEQWVNFPEGEKV 80
Db    350 YSPDNGKRVDVKLTKEEVASWKTDGVLLNGKILTGRTDAHKRL-----VDMLDKGEEEL 404
QY    81 HIE 83
Db    405 PVD 407

RESULT 8
US-11-516-230-44271
; Sequence 44271, Application US/11516230
; Publication No. US20070118916A1
; GENERAL INFORMATION:
; APPLICANT: Plesch, Gunnar
; APPLICANT: Puzio, Piotr
; APPLICANT: Blau, Astrid
; APPLICANT: Herold, Manfred
; APPLICANT: Wendel, Birgit
; APPLICANT: Kamlage, Beate
; APPLICANT: Schaecker, Florian
; APPLICANT: Looser, Ralf
; TITLE OF INVENTION: Process for the production of fine chemicals
; FILE REFERENCE: 13195-00014-US
; CURRENT APPLICATION NUMBER: US/11/516,230
; CURRENT FILING DATE: 2006-09-06
; PRIOR APPLICATION NUMBER: EP 06110426.1
; PRIOR FILING DATE: 2006-02-24
; PRIOR APPLICATION NUMBER: EP 06110579.7
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 73449
; SOFTWARE: Biomax PatentTool according to PatentIN 3.1 format
; SEQ ID NO 44265
; LENGTH: 546
; TYPE: PR1
; ORGANISM: Neisseria meningitidis Z2491
US-11-516-230-44265

Query Match      16.0%; Score 78; DB 7; Length 546;
Best Local Similarity 30.2%; Pred.No. 14;
Matches 19; Conservative 18; Mismatches 2
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OTHER INFORMATION: n is a o r g o r t.
FEATURE:
NAME/KEY: misc feature
LOCATION: (786944)..(786946)
OTHER INFORMATION: n is a o r g o r t.
FEATURE:
NAME/KEY: misc feature
LOCATION: (839139)..(839139)
OTHER INFORMATION: n is a o r g o r t.
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NAME/KEY: misc feature
LOCATION: (1128488)..(1128488)
OTHER INFORMATION: n is a o r g o r t.
FEATURE:
NAME/KEY: misc feature
LOCATION: (1128499)..(1128499)
OTHER INFORMATION: n is a o r g o r t.
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NAME/KEY: misc feature
LOCATION: (1128505)..(1128506)
OTHER INFORMATION: n is a o r g o r t.
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NAME/KEY: misc feature
LOCATION: (1128517)..(1128518)
OTHER INFORMATION: n is a o r g o r t.
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NAME/KEY: misc feature
LOCATION: (1128539)..(1128540)
OTHER INFORMATION: n is a o r g o r t.
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NAME/KEY: misc feature
LOCATION: (1561400)..(1561400)
OTHER INFORMATION: n is a o r g o r t.
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NAME/KEY: misc feature
LOCATION: (1561477)..(1561477)
OTHER INFORMATION: n is a o r g o r t.
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NAME/KEY: misc feature
LOCATION: (1561545)..(1561545)
OTHER INFORMATION: n is a o r g o r t.
FEATURE:
NAME/KEY: misc feature
LOCATION: (1767941)..(1767941)
OTHER INFORMATION: n is a o r g o r t.
US-10-526-324-706

Query Match 15.4%; Score 75; DB 6; Length 309;
Best Local Similarity 30.0%; Pred. No. 15;
Matches 24; Conservative 13; Mismatches 29; Indels 14; Gaps 2;

QY 15 EGQDFQLYPGE-----LGKRIYNEISKEAWAQHQTMLINE-----KKLNMWNA 60
DB 111 EKTDHVLLIGGAVKFAFLLIGFEDYPTTEERLKQWEELRKKLIEKGETYHKWKKLNLIK 170
QY 61 EHRKLEQEMVNFLEFEGKEV 80
DB 171 EYPEVLSTVGAVFDGEEV 190

RESULT 10
US-10-419-128-24473
Sequence 24473, Application US/10419128
Publication No. US20070020624A1
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/10/419,128
CURRENT FILING DATE: 2003-04-21
PRIOR APPLICATION NUMBER: US/09/252,991
PRIOR FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 24473
LENGTH: 474
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-10-419-128-24473

Query Match 14.8%; Score 72; DB 6; Length 474;
Best Local Similarity 25.6%; Pred. No. 50;
Matches 20; Conservative 18; Mismatches 28; Indels 12; Gaps 3;
QY 13 EAEQDFQLYP-----GELGKRI-YNEISKEAWAQHQTMLINEKKLNMWNAEHRKL 65
DB 299 ELEAPSLDAYPEIVWEAGPSARRVDLDKITPEEVQSKPGETLLNGKMLTGRDAHAKR- 357
QY 66 LEQEMVNFLEFEGKEVHIE 83
DB 358 ----MVDMLNKGETLPVD 371

RESULT 11
US-11-516-230-44261
Sequence 44261, Application US/11516230
Publication No. US20070118916A1
GENERAL INFORMATION:
APPLICANT: Plesch, Gunnar
APPLICANT: Puzio, Piotr
APPLICANT: Blau, Astrid
APPLICANT: Herold, Manfred
APPLICANT: Wendel, Birgit
APPLICANT: Kamlage, Beate
APPLICANT: Schauwecker, Florian
APPLICANT: Looser, Ralf
TITLE OF INVENTION: Process for the production of fine chemicals
FILE REFERENCE: 13195-00014-US
CURRENT APPLICATION NUMBER: US/11/516,230
CURRENT FILING DATE: 2006-09-06
PRIOR APPLICATION NUMBER: EP 06110426.1
PRIOR FILING DATE: 2006-02-24
PRIOR APPLICATION NUMBER: EP 06110579.7
PRIOR FILING DATE: 2006-02-28
PRIOR APPLICATION NUMBER: EP 06110425.3
PRIOR FILING DATE: 2006-02-24
PRIOR APPLICATION NUMBER: EP 06110423.8
PRIOR FILING DATE: 2006-02-24
PRIOR APPLICATION NUMBER: EP 06110418.8
PRIOR FILING DATE: 2006-02-24
PRIOR APPLICATION NUMBER: EP 06110383.4
PRIOR FILING DATE: 2006-02-24
PRIOR APPLICATION NUMBER: EP 06110378.4
PRIOR FILING DATE: 2006-02-24
PRIOR APPLICATION NUMBER: EP 06110367.7
PRIOR FILING DATE: 2006-02-24
PRIOR APPLICATION NUMBER: EP 06110327.1
PRIOR FILING DATE: 2006-02-23
PRIOR APPLICATION NUMBER: EP 06110325.5
PRIOR FILING DATE: 2006-02-23
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 73449
SOFTWARE: Biomax PatentTool according to PatentIN 3.1 format
SEQ ID NO 44261
LENGTH: 507
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa PA01
US-11-516-230-44261

Query Match 14.8%; Score 72; DB 7; Length 507;
Best Local Similarity 25.6%; Pred. No. 54;
Matches 20; Conservative 18; Mismatches 28; Indels 12; Gaps 3;

QY 13 EAGQDFQLYP-----GELGKRI-YNEISKEAWAQHQTMLINEKLNMMNAEHRKL 65
Db 294 ELEAPSLDAYPELWVAGPSARVDLKITPEEVQSKPGETILLNGKMLTGRDAAHKR- 352
QY 66 LEQEMVNFLEPGKEVHIE 83
Db 353 ----WVDMLNKGETLPVD 366

RESULT 12
US-10-703-032-118890
; Sequence 118890, Application US/10703032
; Publication No. US20070044171A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Andersen, Scott E.
; APPLICANT: Byrum, Joseph R.
; APPLICANT: Conner, Timothy W.
; APPLICANT: Cao, Yongwei
; APPLICANT: Masucci, James D.
; APPLICANT: Zhou, Yihua
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated with
; FILE REFERENCE: 38-21(53374)B
; CURRENT APPLICATION NUMBER: US/10/703,032
; CURRENT FILING DATE: 2003-11-06
; PRIOR APPLICATION NUMBER: 10/020,338
; PRIOR FILING DATE: 2001-12-12
; NUMBER OF SEQ ID NOS: 211164
; SEQ ID NO 118890
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Triticum aestivum
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_TA_13308.pep
US-10-703-032-118890

Query Match 14.7%; Score 71.5; DB 6; Length 118;
Best Local Similarity 25.6%; Pred. No. 11;
Matches 20; Conservative 18; Mismatches 25; Indels 15; Gaps 2;
QY 9 FLOREAGQDFQLYPGELGKRIYNEISKEAWAQHQTMLINEKLNMMNAEHRKL 68
Db 22 FLPLQGGGRYIRLPQSVSEDL-----PHTETMLNTSQVDLDNIDMNEFPKV 70
QY 69 EMVNR---LFEQKEVHI 82
Db 71 ENLDFMDCILEGDMLEYI 88

RESULT 13
US-10-276-817B-12931
; Sequence 12931, Application US/10276817B
; Publication No. US20070060743A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-104
; CURRENT APPLICATION NUMBER: US/10/276,817B
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: PCT/US01/14827
; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/577,408
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 16102
; SOFTWARE: Custom
; SEQ ID NO 12931
; LENGTH: 566
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN

; LOCATION: (304)..(352)
; OTHER INFORMATION: Intermediate filaments proteins domain identified by eMATRIX.
; OTHER INFORMATION: accession number BL00226B, p-value=6.337e-09, raw score of 23.86
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (400)..(436)
; OTHER INFORMATION: MYND finger domain identified by Pfam, accession name zf-
; OTHER INFORMATION: MYND, E-value=0.0097, Pfam score of 10.4
US-10-276-817B-12931

Query Match 14.7%; Score 71.5; DB 6; Length 566;
Best Local Similarity 28.9%; Pred. No. 70;
Matches 24; Conservative 10; Mismatches 28; Indels 21; Gaps 3;
QY 30 IYNEISKE-AW-----AQWQHQTMLINEKLNMMNAEHRKL 71
Db 311 IYNDLSKNTTWWKAQLAEDSQGLRIEIKLQWLHQQLSEMKHNLLELTWAEKRSLEQERD 370
QY 72 NFLPEGK---EVHIEGYTPEDKK 91
Db 371 RLIAEVKKQLELEKQQAQVDETKK 393

RESULT 14

US-10-917-503-11063
; Sequence 11063, Application US/10917503
; Publication No. US20070105122A1
; GENERAL INFORMATION:
; APPLICANT: OTA, TOSHIO
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: NISHIKAWA, TETSUO
; APPLICANT: HAYASHI, KOJI
; APPLICANT: SAITO, KAORU
; APPLICANT: YAMAMOTO, JUNICHI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: WAKAMATSU, AI
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: OTSUKI, TETSUJI
; TITLE OF INVENTION: PRIMERS FOR SYNTHESIZING FULL-LENGTH CDNA AND THEIR USE
; FILE REFERENCE: 084335/0123
; CURRENT APPLICATION NUMBER: US/10/917,503
; CURRENT FILING DATE: 2004-08-13
; PRIOR APPLICATION NUMBER: US/09/629,469
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: JP 1999-248036
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: JP 1999-300253
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: JP 2000-118776
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: JP 2000-183767
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: JP 2000-241899
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/159,590
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: 60/183,322
; PRIOR FILING DATE: 2000-02-17
; NUMBER OF SEQ ID NOS: 19025
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11063
; LENGTH: 285
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-917-503-11063

Query Match 14.5%; Score 70.5; DB 6; Length 285;
Best Local Similarity 28.4%; Pred. No. 40;
Matches 23; Conservative 10; Mismatches 29; Indels 19; Gaps 2;
QY 30 IYNEISKEAWA-----AQWQHQTMLINEKLNMMNAEHRKL 73
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Db 43 IYDLSKNTTGTIAEIRRLRIEIKLQWLHQOELSEMKNHLELTWAEMRQSLQERDRL 102
QY 74 LFEKG---EVHIEGYTPEDKK 91
Db 103 IAEVKKOLELEKQQAQVDETKK 123

RESULT 15
US-11-443-428A-890387
; Sequence 890387, Application US/11443428A
; Publication No. US20070083334A1
; GENERAL INFORMATION:
; APPLICANT: Mintz, Liat
; APPLICANT: Xie, Hanqing
; APPLICANT: Dahari, Dvir
; APPLICANT: Levanon, Erez
; APPLICANT: Freilich, Shiri
; APPLICANT: Beck, Nili
; APPLICANT: Zhu, Wei-Yong
; APPLICANT: Wasserman, Alon
; APPLICANT: Hermesh, Chen
; APPLICANT: Azar, Idit
; APPLICANT: Bernstein, Jeanne
; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
; FILE REFERENCE: 02/23929
; CURRENT APPLICATION NUMBER: US/11/443,428A
; CURRENT FILING DATE: 2006-05-31
; NUMBER OF SEQ ID NOS: 1034312
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 890387
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-443-428A-890387

Query Match 14.5%; Score 70.5; DB 7; Length 313;
Best Local Similarity 28.4%; Pred. No. 44;
Matches 23; Conservative 10; Mismatches 29; Indels 19; Gaps 2;

QY 30 IYNEISKEAWA-----OWOHKOTMLINEKKLNMMNAEHRKLLQEOMVNF 73
Db 43 IYDLSKNTTGTIAEIRRLRIEIKLQWLHQOELSEMKNHLELTWAEMRQSLQERDRL 102
QY 74 LFEKG---EVHIEGYTPEDKK 91
Db 103 IAEVKKOLELEKQQAQVDETKK 123

RESULT 16
US-11-443-428A-890388
; Sequence 890388, Application US/11443428A
; Publication No. US20070083334A1
; GENERAL INFORMATION:
; APPLICANT: Mintz, Liat
; APPLICANT: Xie, Hanqing
; APPLICANT: Dahari, Dvir
; APPLICANT: Levanon, Erez
; APPLICANT: Freilich, Shiri
; APPLICANT: Beck, Nili
; APPLICANT: Zhu, Wei-Yong
; APPLICANT: Wasserman, Alon
; APPLICANT: Hermesh, Chen
; APPLICANT: Azar, Idit
; APPLICANT: Bernstein, Jeanne
; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
; FILE REFERENCE: 02/23929
; CURRENT APPLICATION NUMBER: US/11/443,428A
; CURRENT FILING DATE: 2006-05-31
; NUMBER OF SEQ ID NOS: 1034312
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 890388
; LENGTH: 313
; TYPE: PRT
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; ORGANISM: Homo sapiens
US-11-443-428A-890388

Query Match 14.5%; Score 70.5; DB 7; Length 313;
Best Local Similarity 28.4%; Pred. No. 44;
Matches 23; Conservative 10; Mismatches 29; Indels 19; Gaps 2;

QY 30 IYNEISKEAWA-----OWOHKOTMLINEKKLNMMNAEHRKLLQEOMVNF 73
Db 43 IYDLSKNTTGTIAEIRRLRIEIKLQWLHQOELSEMKNHLELTWAEMRQSLQERDRL 102
QY 74 LFEKG---EVHIEGYTPEDKK 91
Db 103 IAEVKKOLELEKQQAQVDETKK 123

RESULT 17
US-10-567-867-1402
; Sequence 1402, Application US/10567867
; Publication No. US20070105114A1
; GENERAL INFORMATION:
; APPLICANT: Li, Martha
; APPLICANT: Rupnow, Brent A.
; APPLICANT: Webster, Kevin R.
; APPLICANT: Jackson, Donald
; APPLICANT: Wong, Tai W.
; TITLE OF INVENTION: BIOMARKERS OF CYCLIN-DEPENDENT KINASE MODULATION
; FILE REFERENCE: D0310 PCT
; CURRENT APPLICATION NUMBER: US/10/567,867
; CURRENT FILING DATE: 2006-01-27
; PRIOR APPLICATION NUMBER: US 60/490,890
; PRIOR FILING DATE: 2003-07-29
; NUMBER OF SEQ ID NOS: 2786
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1402
; LENGTH: 614
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-567-867-1402

Query Match 14.5%; Score 70.5; DB 6; Length 614;
Best Local Similarity 28.4%; Pred. No. 97;
Matches 23; Conservative 10; Mismatches 29; Indels 19; Gaps 2;

QY 30 IYNEISKEAWA-----OWOHKOTMLINEKKLNMMNAEHRKLLQEOMVNF 73
Db 372 IYDLSKNTTGTIAEIRRLRIEIKLQWLHQOELSEMKNHLELTWAEMRQSLQERDRL 431
QY 74 LFEKG---EVHIEGYTPEDKK 91
Db 432 IAEVKKOLELEKQQAQVDETKK 452

RESULT 18
US-11-443-428A-890383
; Sequence 890383, Application US/11443428A
; Publication No. US20070083334A1
; GENERAL INFORMATION:
; APPLICANT: Mintz, Liat
; APPLICANT: Xie, Hanqing
; APPLICANT: Dahari, Dvir
; APPLICANT: Levanon, Erez
; APPLICANT: Freilich, Shiri
; APPLICANT: Beck, Nili
; APPLICANT: Zhu, Wei-Yong
; APPLICANT: Wasserman, Alon
; APPLICANT: Hermesh, Chen
; APPLICANT: Azar, Idit
; APPLICANT: Bernstein, Jeanne
; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
; FILE REFERENCE: 02/23929
; CURRENT APPLICATION NUMBER: US/11/443,428A
; CURRENT FILING DATE: 2006-05-31
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; NUMBER OF SEQ ID NOS: 1034312
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 890383
; LENGTH: 647
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-443-428A-890383

Query Match      14.5%; Score 70.5; DB 7; Length 647;
Best Local Similarity 28.4%; Pred. No. 1.e+02;
Matches 23; Conservative 10; Mismatches 29; Indels 19; Gaps 2;

QY 30 IYNEISKEAWA-----OWOHKOTMLINEKLNMMNAEHRKLLQEWMVNF 73
Db 405 IYNDLSKNTTGSTIAIRLRIRIEIKLQWLHQOELSEMKNHLELTWAEWRQSLQEQRDL 464

QY 74 LPEGK---EVHIEGYTPEDKK 91
Db 465 IAEVKKQLELEKQQAQVDETKK 485

RESULT 19
US-10-405-027-3329
; Sequence 3329, Application US/10405027
; Publication No. US20070015271A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: PS806PI
; CURRENT APPLICATION NUMBER: US/10/405,027
; CURRENT FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: 60/369,608
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 60/376,175
; PRIOR FILING DATE: 2002-04-30
; NUMBER OF SEQ ID NOS: 5810
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3329
; LENGTH: 702
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (4)
; OTHER INFORMATION: Xaa equals any amino acid
US-10-405-027-3329

Query Match      14.5%; Score 70.5; DB 6; Length 702;
Best Local Similarity 28.4%; Pred. No. 1.le+02;
Matches 23; Conservative 10; Mismatches 29; Indels 19; Gaps 2;

QY 30 IYNEISKEAWA-----OWOHKOTMLINEKLNMMNAEHRKLLQEWMVNF 73
Db 432 IYNDLSKNTTGSTIAIRLRIRIEIKLQWLHQOELSEMKNHLELTWAEWRQSLQEQRDL 491

QY 74 LPEGK---EVHIEGYTPEDKK 91
Db 492 IAEVKKQLELEKQQAQVDETKK 512

RESULT 20
US-11-582-861-6676
; Sequence 6676, Application US/11582861
; Publication No. US20070099251A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Hui
; APPLICANT: Aebersold, Rudolf H.
; TITLE OF INVENTION: TISSUE- AND SERUM-DERIVED GLYCOPROTEINS
; TITLE OF INVENTION: AND METHODS OF THEIR USE
; FILE REFERENCE: 460092.404
; CURRENT APPLICATION NUMBER: US/11/582,861
; CURRENT FILING DATE: 2006-10-17
; PRIOR APPLICATION NUMBER: 60/728,044
; OTHER INFORMATION: Xaa equals any amino acid
US-11-582-861-6676

; NUMBER OF SEQ ID NOS: 1034312
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 890383
; LENGTH: 647
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-443-428A-890383

Query Match      14.5%; Score 70.5; DB 7; Length 647;
Best Local Similarity 28.4%; Pred. No. 1.e+02;
Matches 23; Conservative 10; Mismatches 29; Indels 19; Gaps 2;

QY 30 IYNEISKEAWA-----OWOHKOTMLINEKLNMMNAEHRKLLQEWMVNF 73
Db 405 IYNDLSKNTTGSTIAIRLRIRIEIKLQWLHQOELSEMKNHLELTWAEWRQSLQEQRDL 464

QY 74 LPEGK---EVHIEGYTPEDKK 91
Db 465 IAEVKKQLELEKQQAQVDETKK 485

RESULT 19
US-10-405-027-3329
; Sequence 3329, Application US/10405027
; Publication No. US20070015271A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: PS806PI
; CURRENT APPLICATION NUMBER: US/10/405,027
; CURRENT FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: 60/369,608
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 60/376,175
; PRIOR FILING DATE: 2002-04-30
; NUMBER OF SEQ ID NOS: 5810
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3329
; LENGTH: 702
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (4)
; OTHER INFORMATION: Xaa equals any amino acid
US-10-405-027-3329

Query Match      14.5%; Score 70.5; DB 6; Length 702;
Best Local Similarity 28.4%; Pred. No. 1.le+02;
Matches 23; Conservative 10; Mismatches 29; Indels 19; Gaps 2;

QY 30 IYNEISKEAWA-----OWOHKOTMLINEKLNMMNAEHRKLLQEWMVNF 73
Db 432 IYNDLSKNTTGSTIAIRLRIRIEIKLQWLHQOELSEMKNHLELTWAEWRQSLQEQRDL 491

QY 74 LPEGK---EVHIEGYTPEDKK 91
Db 492 IAEVKKQLELEKQQAQVDETKK 512

RESULT 20
US-11-582-861-6676
; Sequence 6676, Application US/11582861
; Publication No. US20070099251A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Hui
; APPLICANT: Aebersold, Rudolf H.
; TITLE OF INVENTION: TISSUE- AND SERUM-DERIVED GLYCOPROTEINS
; TITLE OF INVENTION: AND METHODS OF THEIR USE
; FILE REFERENCE: 460092.404
; CURRENT APPLICATION NUMBER: US/11/582,861
; CURRENT FILING DATE: 2006-10-17
; PRIOR APPLICATION NUMBER: 60/728,044
; OTHER INFORMATION: Xaa equals any amino acid
US-11-582-861-6676

; PRIOR FILING DATE: 2005-10-17
; NUMBER OF SEQ ID NOS: 14918
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6676
; LENGTH: 764
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-582-861-6676

Query Match      14.5%; Score 70.5; DB 7; Length 764;
Best Local Similarity 28.4%; Pred. No. 1.3e+02;
Matches 23; Conservative 10; Mismatches 29; Indels 19; Gaps 2;

QY 30 IYNEISKEAWA-----OWOHKOTMLINEKLNMMNAEHRKLLQEWMVNF 73
Db 522 IYNDLSKNTTGSTIAIRLRIRIEIKLQWLHQOELSEMKNHLELTWAEWRQSLQEQRDL 581

QY 74 LPEGK---EVHIEGYTPEDKK 91
Db 582 IAEVKKQLELEKQQAQVDETKK 602

RESULT 21
US-11-582-861-6675
; Sequence 6675, Application US/11582861
; Publication No. US20070099251A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Hui
; APPLICANT: Aebersold, Rudolf H.
; TITLE OF INVENTION: TISSUE- AND SERUM-DERIVED GLYCOPROTEINS
; TITLE OF INVENTION: AND METHODS OF THEIR USE
; FILE REFERENCE: 460092.404
; CURRENT APPLICATION NUMBER: US/11/582,861
; CURRENT FILING DATE: 2006-10-17
; PRIOR APPLICATION NUMBER: 60/728,044
; PRIOR FILING DATE: 2005-10-17
; NUMBER OF SEQ ID NOS: 14918
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6675
; LENGTH: 995
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-582-861-6675

Query Match      14.5%; Score 70.5; DB 7; Length 995;
Best Local Similarity 28.4%; Pred. No. 1.7e+02;
Matches 23; Conservative 10; Mismatches 29; Indels 19; Gaps 2;

QY 30 IYNEISKEAWA-----OWOHKOTMLINEKLNMMNAEHRKLLQEWMVNF 73
Db 753 IYNDLSKNTTGSTIAIRLRIRIEIKLQWLHQOELSEMKNHLELTWAEWRQSLQEQRDL 812

QY 74 LPEGK---EVHIEGYTPEDKK 91
Db 813 IAEVKKQLELEKQQAQVDETKK 833

RESULT 22
US-11-443-428A-890379
; Sequence 890379, Application US/11443428A
; Publication No. US2007008334A1
; GENERAL INFORMATION:
; APPLICANT: Mintz, Liat
; APPLICANT: Xie, Hanning
; APPLICANT: Dahari, Dvir
; APPLICANT: Levanon, Erez
; APPLICANT: Freilich, Shiri
; APPLICANT: Beck, Nili
; APPLICANT: Zhu, Wei-Yong
; APPLICANT: Wasserman, Alon
; APPLICANT: Hermesh, Chen
; APPLICANT: Azar, Idit
; APPLICANT: Bernstein, Jeanne
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; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
; FILE REFERENCE: 02/23929
; CURRENT APPLICATION NUMBER: US/11/443,428A
; CURRENT FILING DATE: 2006-05-31
; NUMBER OF SEQ ID NOS: 1034312
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 890379
; LENGTH: 1072
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-443-428A-890379

Query Match          14.5%; Score 70.5; DB 7; Length 1072;
Best Local Similarity 28.4%; Pred. No. 1.9e+02;
Matches 23; Conservative 10; Mismatches 29; Indels 19; Gaps 2;

QY 30 IYNEISKEAWA-----QWQHKOTMLINEKLNMMNAEHRKLLQEWMVNF 73
      |||:|:|
Db 830 IYNDLSKNTGTSTIAIRRLRIEIKLQWLHQQLSEMKHNLELTMAEMRQSLQEQRDL 889
      |||:|:|

QY 74 LFEKG---EVHIEGYTPEDKK 91
      :|:|:|
Db 890 IAEVKKQLEKQQAQVDETKK 910

RESULT 23
US-11-443-428A-890395
; Sequence 890395, Application US/11443428A
; Publication No. US2007008334A1
; GENERAL INFORMATION:
; APPLICANT: Mintz, Liat
; APPLICANT: Xie, Hanqing
; APPLICANT: Dahari, Dvir
; APPLICANT: Levanon, Erez
; APPLICANT: Freilich, Shiri
; APPLICANT: Beck, Nili
; APPLICANT: Zhu, Wei-Yong
; APPLICANT: Wasserman, Alon
; APPLICANT: Hermesh, Chen
; APPLICANT: Azar, Idit
; APPLICANT: Bernstein, Jeanne
; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
; FILE REFERENCE: 02/23929
; CURRENT APPLICATION NUMBER: US/11/443,428A
; CURRENT FILING DATE: 2006-05-31
; NUMBER OF SEQ ID NOS: 1034312
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 890395
; LENGTH: 1072
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-443-428A-890395

Query Match          14.5%; Score 70.5; DB 7; Length 1072;
Best Local Similarity 28.4%; Pred. No. 1.9e+02;
Matches 23; Conservative 10; Mismatches 29; Indels 19; Gaps 2;

QY 30 IYNEISKEAWA-----QWQHKOTMLINEKLNMMNAEHRKLLQEWMVNF 73
      |||:|:|
Db 830 IYNDLSKNTGTSTIAIRRLRIEIKLQWLHQQLSEMKHNLELTMAEMRQSLQEQRDL 889
      |||:|:|

QY 74 LFEKG---EVHIEGYTPEDKK 91
      :|:|:|
Db 890 IAEVKKQLEKQQAQVDETKK 910

RESULT 24
US-11-443-428A-890399
; Sequence 890399, Application US/11443428A
; Publication No. US2007008334A1
; GENERAL INFORMATION:
; APPLICANT: Mintz, Liat
; APPLICANT: Xie, Hanqing
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; APPLICANT: Dahari, Dvir
; APPLICANT: Levanon, Erez
; APPLICANT: Freilich, Shiri
; APPLICANT: Beck, Nili
; APPLICANT: Zhu, Wei-Yong
; APPLICANT: Wasserman, Alon
; APPLICANT: Hermesh, Chen
; APPLICANT: Azar, Idit
; APPLICANT: Bernstein, Jeanne
; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
; FILE REFERENCE: 02/23929
; CURRENT APPLICATION NUMBER: US/11/443,428A
; CURRENT FILING DATE: 2006-05-31
; NUMBER OF SEQ ID NOS: 1034312
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 890399
; LENGTH: 1107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-443-428A-890399

Query Match          14.5%; Score 70.5; DB 7; Length 1107;
Best Local Similarity 28.4%; Pred. No. 1.9e+02;
Matches 23; Conservative 10; Mismatches 29; Indels 19; Gaps 2;

QY 30 IYNEISKEAWA-----QWQHKOTMLINEKLNMMNAEHRKLLQEWMVNF 73
      |||:|:|
Db 837 IYNDLSKNTGTSTIAIRRLRIEIKLQWLHQQLSEMKHNLELTMAEMRQSLQEQRDL 896
      |||:|:|

QY 74 LFEKG---EVHIEGYTPEDKK 91
      :|:|:|
Db 897 IAEVKKQLEKQQAQVDETKK 917

RESULT 25
US-11-443-428A-890396
; Sequence 890396, Application US/11443428A
; Publication No. US2007008334A1
; GENERAL INFORMATION:
; APPLICANT: Mintz, Liat
; APPLICANT: Xie, Hanqing
; APPLICANT: Dahari, Dvir
; APPLICANT: Levanon, Erez
; APPLICANT: Freilich, Shiri
; APPLICANT: Beck, Nili
; APPLICANT: Zhu, Wei-Yong
; APPLICANT: Wasserman, Alon
; APPLICANT: Hermesh, Chen
; APPLICANT: Azar, Idit
; APPLICANT: Bernstein, Jeanne
; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
; FILE REFERENCE: 02/23929
; CURRENT APPLICATION NUMBER: US/11/443,428A
; CURRENT FILING DATE: 2006-05-31
; NUMBER OF SEQ ID NOS: 1034312
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 890396
; LENGTH: 1115
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-443-428A-890396

Query Match          14.5%; Score 70.5; DB 7; Length 1115;
Best Local Similarity 28.4%; Pred. No. 1.9e+02;
Matches 23; Conservative 10; Mismatches 29; Indels 19; Gaps 2;

QY 30 IYNEISKEAWA-----QWQHKOTMLINEKLNMMNAEHRKLLQEWMVNF 73
      |||:|:|
Db 873 IYNDLSKNTGTSTIAIRRLRIEIKLQWLHQQLSEMKHNLELTMAEMRQSLQEQRDL 932
      |||:|:|

QY 74 LFEKG---EVHIEGYTPEDKK 91
      :|:|:|
Db 933 IAEVKKQLEKQQAQVDETKK 953
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